

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:08:27 ; Search time 19 Seconds
(without alignments)
1130.337 Million cell updates/sec

Title: US-09-961-201A-1
Perfect score: 416
Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKQMPGCFNFKLFFKTS 416

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/prodata/2/iaa/PCFUS COMB.pep.*
- 6: /cgn2_6/prodata/2/iaa/backfilees1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query	DB ID	Description
1	416	100.0	416	3	US-08-852-936C-1
2	416	100.0	416	3	US-09-300-328-1
3	416	100.0	416	4	US-09-069-023-23
4	219	52.6	416	4	US-09-561-756-30
5	219	52.6	416	4	US-09-227-721-30
6	219	52.6	416	4	US-09-954-697-30
7	202	48.6	203	3	US-08-852-936C-4
8	202	48.6	203	3	US-09-300-328-4
9	195	46.9	416	3	US-09-257-218-2
10	195	46.9	416	3	US-09-311-760-2
11	195	46.9	416	4	US-08-865-579-2
12	195	46.9	416	4	US-10-059-749-2
13	15	3.6	15	3	US-09-257-218-22
14	15	3.6	15	3	US-09-311-760-22
15	15	3.6	15	4	US-09-561-756-59
16	15	3.6	15	4	US-09-227-721-59
17	15	3.6	15	4	US-08-865-579-22
18	15	3.6	15	4	US-10-059-749-22
19	15	3.6	46	3	US-09-954-697-59
20	15	3.6	46	3	US-09-257-218-6
21	15	3.6	46	3	US-09-311-760-6
22	15	3.6	46	4	US-08-865-579-6
23	15	3.6	46	4	US-10-059-749-6
24	11	2.4	299	2	US-08-773-688A-2
25	10	2.4	39	4	US-09-187-789-38
26	10	2.4	39	4	US-09-139-600-33
27	10	2.4	303	3	US-08-462-969B-2

28	10	2.4	303	4	US-09-561-756-24	Sequence 24, Appl
29	10	2.4	303	4	US-09-227-721-24	Sequence 24, Appl
30	10	2.4	303	4	US-08-556-627A-2	Sequence 2, Appl
31	10	2.4	303	4	US-09-124-934A-2	Sequence 2, Appl
32	10	2.4	303	4	US-08-724-378D-4	Sequence 4, Appl
33	10	2.4	303	4	US-08-334-251D-2	Sequence 2, Appl
34	10	2.4	303	4	US-09-954-697-24	Sequence 24, Appl
35	10	2.4	303	4	US-09-163-099-2	Sequence 2, Appl
36	10	2.4	346	2	US-08-618-408B-2	Sequence 2, Appl
37	10	2.4	389	4	US-08-724-378D-2	Sequence 2, Appl
38	10	2.4	389	4	US-08-665-220-2	Sequence 3, Appl
39	10	2.4	479	1	US-08-724-378D-3	Sequence 2, Appl
40	10	2.4	479	3	US-09-291-692-2	Sequence 3, Appl
41	10	2.4	479	4	US-09-561-756-33	Sequence 2, Appl
42	10	2.4	479	4	US-09-227-721-33	Sequence 33, Appl
43	10	2.4	479	4	US-09-954-697-33	Sequence 4, Appl
44	10	2.4	479	4	US-09-009-893A-4	Sequence 2, Appl
45	10	2.4	479	4	US-09-489-155-4	Sequence 4, Appl
46	10	2.4	521	4	US-09-962-834A-2	Sequence 2, Appl
47	9	2.2	9	3	US-09-257-218-19	Sequence 19, Appl
48	9	2.2	9	3	US-09-311-760-19	Sequence 19, Appl
49	9	2.2	9	4	US-09-561-756-56	Sequence 56, Appl
50	9	2.2	9	4	US-09-227-721-56	Sequence 56, Appl
51	9	2.2	9	4	US-08-865-579-19	Sequence 19, Appl
52	9	2.2	9	4	US-10-059-749-19	Sequence 19, Appl
53	9	2.2	9	4	US-09-954-697-56	Sequence 56, Appl
54	9	2.2	1196	3	US-08-801-706-2	Sequence 2, Appl
55	8	1.9	141	4	US-09-252-991A-16951	Sequence 16951, A
56	8	1.9	1218	4	US-09-198-452A-98	Sequence 98, Appl
57	7	1.7	25	4	US-09-257-179-96	Sequence 96, Appl
58	7	1.7	141	4	US-09-252-991A-25224	Sequence 25224, A
59	7	1.7	150	4	US-09-198-452A-1023	Sequence 1023, Ap
60	7	1.7	202	4	US-09-257-179-90	Sequence 90, Appl
61	7	1.7	248	4	US-09-252-991A-23249	Sequence 23249, A
62	7	1.7	253	4	US-09-252-991A-22878	Sequence 22878, A
63	7	1.7	304	4	US-09-252-991A-23222	Sequence 23222, A
64	7	1.7	313	4	US-09-252-991A-30181	Sequence 30181, A
65	7	1.7	318	4	US-09-292-858B-24	Sequence 24, Appl
66	7	1.7	324	4	US-09-328-352-6612	Sequence 6612, Ap
67	7	1.7	339	4	US-09-252-991A-27733	Sequence 27733, A
68	7	1.7	358	4	US-09-489-039A-9326	Sequence 9326, A
69	7	1.7	369	4	US-09-252-991A-23356	Sequence 23356, A
70	7	1.7	373	4	US-09-489-039A-11774	Sequence 11774, A
71	7	1.7	401	1	US-08-198-446B-11	Sequence 11, Appl
72	7	1.7	401	2	US-08-870-693-11	Sequence 11, Appl
73	7	1.7	419	4	US-09-134-001C-3441	Sequence 3441, Ap
74	7	1.7	423	4	US-09-328-352-6273	Sequence 6273, Ap
75	7	1.7	426	4	US-09-252-991A-29288	Sequence 29288, A

ALIGNMENTS

RESULT 1
US-08-852-936C-1
; Sequence 1, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:

APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
AGENT OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,328
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/852,936
FILING DATE: 08-MAY-1997
APPLICATION NUMBER: 60/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
09-300-328-1

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852.936C
FILING DATE: 08-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031

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; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-936C-1

Query Match          100.0%; Score 416; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDADRRLLRRLRLRVLEELQVDQLMDVLLSRFLFRPHMTIEDQRAGSGSRRDQARQLII 60
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Db       1 MDEADRLLRRLRLRVLEELQVDQLMDVLLSRFLFRPHMTIEDQRAGSGSRRDQARQLII 60
        |||

QY      61 DLETGRSQALPLFISCLEDTGQDMLASFLTNRNQAGLSKPTLENLTPVVLRPEIRKPEV 120
        |||
Db       61 DLETGRSQALPLFISCLEDTGQDMLASFLTNRNQAGLSKPTLENLTPVVLRPEIRKPEV 120
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QY	121	LRPETRPVDIGSGGFDVGALSLRGNADLAILSMPEPCGCHCLLIINNANFPCRESGLR	180
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QY	181	TGSNIDCEKLRPRFSSLHFVVEVKGDLTAKMWLALLELARQDHDGALDCCVVWILSHGCQ	240
Db	181	TGSNIDCEKLRPRFSSLHFVVEVKGDLTAKMWLALLELARQDHDGALDCCVVWILSHGCQ	240
QY	241	ASHLQPFQAVYGTGCPVSVKEKVINIENGTSCPSLGGKPKLFFTQACGGEOKDHGFVAS	300
Db	241	ASHLQPFQAVYGTGCPVSVKEKVINIENGTSCPSLGGKPKLFFTQACGGEOKDHGFVAS	300
QY	301	TSPEDSPGSGNPEPDATPFQEGRLTFQDLDAISSLPTPSDIFVSYSTFPFGVSVMRDPKSG	360
Db	301	TSPEDSPGSGNPEPDATPFQEGRLTFQDLDAISSLPTPSDIFVSYSTFPFGVSVMRDPKSG	360
QY	361	SWVETLDDIDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCGCNFLRKKLFFKTS	416
Db	361	SWVETLDDIDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCGCNFLRKKLFFKTS	416

RESULT 2

US-09-300-328-1

; Sequence 1, Application US/09300328

; Patent No. 6294169

; GENERAL INFORMATION:

; APPLICANT: DIXIT, VISHVA M.

; APPLICANT: HE, WEI-WU

; APPLICANT: KIKLY, KRISTINE K.

QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 3

US-09-069-023-23
; Sequence 30, Application US/09069023A
; Patent No. 6348573

GENERAL INFORMATION

; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 23

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-23

Query Match 100.0%; Score 416; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVLDQWLVLSRELFRPHMIEDIQAGSGRRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEELQVLDQWLVLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGQALPLFISCLEDTGQDMLASFLTRNQAGKLSKPTLENLTPVVLREIRKPEV 120

Db 61 DLETRGQALPLFISCLEDTGQDMLASFLTRNQAGKLSKPTLENLTPVVLREIRKPEV 120

QY 121 LRPEPRPVDIGSGGVDGVALSRLGNADLAVILSMPECGHCLIIINNVCRESGLRTR 180

Db 121 LRPEPRPVDIGSGGVDGVALSRLGNADLAVILSMPECGHCLIIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSSLHFMEVVKGLTAKKMWLALLELARQDHGALDCVWVILSHGCO 240

Db 181 TGSNIDCEKLRFRFSSLHFMEVVKGLTAKKMWLALLELARQDHGALDCVWVILSHGCO 240

QY 241 ASHLQPPGAVYCTDGCPSVSEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300

Db 241 ASHLQPPGAVYCTDGCPSVSEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300

QY 301 TSPEDSPGSGNPEPDATPFQEGRLTFDQDLDAISSLPTPSDIFVSYSTPFGFVSWRDPKSG 360

Db 301 TSPEDSPGSGNPEPDATPFQEGRLTFDQDLDAISSLPTPSDIFVSYSTPFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 4

US-09-561-756-30

; Sequence 30, Application US/09561756

; Patent No. 6376226

GENERAL INFORMATION

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/561,756

; CURRENT FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 09/227,721

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-561-756-30

Query Match

Best Local Similarity 100.0%; Pred. No. 8.1e-203;

Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCVWVILSHGCOASHLOFPFGAVYGTDCGP 257

Db 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCVWVILSHGCOASHLOFPFGAVYGTDCGP 257

QY 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317

Db 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317

QY 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHS 377

Db 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHS 377

QY 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

Db 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 5

US-09-227-721-30

; Sequence 30, Application US/09227721

; Patent No. 6379950

GENERAL INFORMATION

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/227,721

; CURRENT FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-227-721-30

Query Match

Best Local Similarity 100.0%; Pred. No. 8.1e-203;

Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCVWVILSHGCOASHLOFPFGAVYGTDCGP 257

Db 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCVWVILSHGCOASHLOFPFGAVYGTDCGP 257

QY 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317

Db 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317

QY 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHS 377

Db 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHS 377

QY 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

Db 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 6

US-09-954-697-30

; Sequence 30, Application US/09954697

; Patent No. 6610541

us-09-961-201a-1.oligo.rai

Tue Aug 3 09:36:12 2004

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; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.43102
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-954-697-30

Query Match      52.6%; Score 219; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 8.1e-203; Indels 0; Gaps 0;
Matches 219; Conservative 0; Mismatches 0;

QY 198 HFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGDCP 257
DB 198 HFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGDCP 257
QY 258 VSVKIVNIFNGTSCPSLGKPKLFFIOACGGEQKDHGFVASTSPEDSGSNPEPDAT 317
DB 258 VSVKIVNIFNGTSCPSLGKPKLFFIOACGGEQKDHGFVASTSPEDSGSNPEPDAT 317
QY 318 PFQGLRTFDQDALISSLPDIFVSYSTPGFVSWDRDPKSGSWYVETLDDIFEQWAHS 377
DB 318 PFQGLRTFDQDALISSLPDIFVSYSTPGFVSWDRDPKSGSWYVETLDDIFEQWAHS 377
QY 378 EDLQSLLLRVANAVSVKGIYKQMPGCNFKLKKLFFKTS 416
DB 378 EDLQSLLLRVANAVSVKGIYKQMPGCNFKLKKLFFKTS 416

; US-08-852-936C-4
; Sequence 4, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936C
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F

```

```

; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-852-936C-4

Query Match      48.6%; Score 202; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-186; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0;

QY 212 MVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTS 271
DB 1 MVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTS 60
QY 272 CPSLGGKPKLFFIOACGGEQKDHGFVASTSPEDSGSNPEPDATPFQGLRTFDQDAL 331
DB 61 CPSLGGKPKLFFIOACGGEQKDHGFVASTSPEDSGSNPEPDATPFQGLRTFDQDAL 120
QY 332 ISSLPDIFVSYSTPGFVSWDRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAV 391
DB 121 ISSLPDIFVSYSTPGFVSWDRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAV 180
QY 392 SVKGIYKQMPGCNFKLKKLFF 413
DB 181 SVKGIYKQMPGCNFKLKKLFF 202

; US-09-300-328-4
; Sequence 4, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,328
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936
; FILING DATE: 08-MAY-1997
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996

```

RESULT 8

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; US-09-300-328-4
; Sequence 4, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,328
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936
; FILING DATE: 08-MAY-1997
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996

```


ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: p50483-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 203 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-300-328-4

Query Match 48.6%; Score 202; DB 3; Length 203;
 Best Local Similarity 100.0%; Pred. No. 1.le-186;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 MVLALLELARQDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVEKIVNIFNGTS 271
 DB 1 MVLALLELARQDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVEKIVNIFNGTS 60
 QY 272 CPSLGGKPKLFFFIQACGGEQKHGFEVASTSPEDSPGSNPEPDATPFQGLRTFDQIDA 331
 DB 61 CPSLGGKPKLFFFIQACGGEQKHGFEVASTSPEDSPGSNPEPDATPFQGLRTFDQIDA 120
 QY 332 ISSLPTSPDIFVSYSTPPGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAV 391
 DB 121 ISSLPTSPDIFVSYSTPPGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAV 180
 QY 392 SVKGIYKQMPGCFNFKLFF 413
 DB 181 SVKGIYKQMPGCFNFKLFF 202

RESULT 9

US-09-257-218-2
 ; Sequence 2, Application US/09257218
 ; Patent No. 6271361
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; APPLICANT: Fernandes-Alnemri, Teresa
 ; APPLICANT: Litwack, Gerald
 ; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 ; TITLE OF INVENTION: Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/257,218
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/865,579
 ; FILING DATE: 29-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-ID 2180
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 416 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-257-218-2

Query Match

Best Local Similarity 46.9%; Score 195; DB 3; Length 416;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVEKIVNIFNGTSCPSLGGKPKL 281
 DB 222 QDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVEKIVNIFNGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEQKHGFEVASTSPEDSPGSNPEPDATPFQGLRTFDQIDAISLPTPSDI 341
 DB 282 FFIQACGGEQKHGFEVASTSPEDSPGSNPEPDATPFQGLRTFDQIDAISLPTPSDI 341
 QY 342 FVSYSTPPGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 DB 342 FVSYSTPPGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNFKLFFKTS 416
 DB 402 GCFNFKLFFKTS 416

RESULT 10

US-09-311-760-2
 ; Sequence 2, Application US/09311760
 ; Patent No. 6274318
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; APPLICANT: Fernandes-Alnemri, Teresa
 ; APPLICANT: Litwack, Gerald
 ; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 ; TITLE OF INVENTION: Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/311,760
 ; FILING DATE: 13-May-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/865,579
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-ID 2180
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-9849
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 416 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

Db 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKHGFEVASTSPEDSPGSGNPPDPATPFQEGRLTFDQDLSLPTPSDI 341
Db 282 FFIQACGGEQKHGFEVASTSPEDSPGSGNPPDPATPFQEGRLTFDQDLSLPTPSDI 341
QY 342 FVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401
Db 342 FVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401
QY 402 GCFNFKLKKLFFKTS 416
Db 402 GCFNFKLKKLFFKTS 416

RESULT 12
US-10-059-749-2
; Sequence 2, Application US/10059749
; Patent No. 656505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; ; Fernandes-Alnemri, Teresa
; ; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; ; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2
Query Match 46.9%; Score 195; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-179; Indels 0; Gaps 0;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKHGFEVASTSPEDSPGSGNPPDPATPFQEGRLTFDQDLSLPTPSDI 341
Db 282 FFIQACGGEQKHGFEVASTSPEDSPGSGNPPDPATPFQEGRLTFDQDLSLPTPSDI 341

QY 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKHGFEVASTSPEDSPGSGNPPDPATPFQEGRLTFDQDLSLPTPSDI 341
Db 282 FFIQACGGEQKHGFEVASTSPEDSPGSGNPPDPATPFQEGRLTFDQDLSLPTPSDI 341
QY 342 FVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401
Db 342 FVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401
QY 402 GCFNFKLKKLFFKTS 416
Db 402 GCFNFKLKKLFFKTS 416

RESULT 11
US-08-865-579-2
; Sequence 2, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; ; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-865-579-2
Query Match 46.9%; Score 195; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-179; Indels 0; Gaps 0;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKL 281

Qy	342	FVSYSTPFQFVSWRPDKSGSWYVETLDDIFEQWAHSEDLSLLIRVANAVSVKGIYKOMP	401
Db	342	FVSYSTPFQFVSWRPDKSGSWYVETLDDIFEQWAHSEDLSLLIRVANAVSVKGIYKOMP	401
Qy	402	GCNFNLKRLFFKTS	416
Db	402	GCNFNLKRLFFKTS	416

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RESULT 13
US/09-257-218-22
; Sequence 22, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218

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Query Match 3.6%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; pred. NO. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels

QY 350 GFVSRDPKSGSWYV 364
Db 1 GFVSRDPKSGSWYV 15

RESULT 14	
US-09-311-760-22	
Sequence 22, Application US/09311760	
Patent No. 6274318	
GENERAL INFORMATION:	
APPLICANT: Alnemri, Emad S.	
Fernandes-Alnemri,	
Litwack, Gerald	
TITLE OF INVENTION: Apoptotic	
Encoding S	

Apoptotic Protease Mch6, Nucleic Acids
Encoding Same and Methods of Use

QY 350 GFVSWRDPKSGSWYV 364
|||
Db 1 GFVSWRDPKSGSWYV 15

NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

Query Match 3.6%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels

QY 350 GFVSWRDPKSGSWYV 364
D_b 1 GFVSWRDPKSGSWYV 15

```

RESULT 15
US-09-561-756-59
; Sequence 59, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; PRIORITY FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-59

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Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15: Conservative 0. Mismatches 0.

Qy 350 GFVSWRDPKSGSWYV 364
 |||||
Db 1 GFVSWRDPKSGSWYV 15

Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 18
US-10-059-749-22
; Sequence 22, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Litwack, Gerald
; Fernandes-Alnemri, Teresa
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749
FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-059-749-22

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 19
US-09-954-697-59
; Sequence 59, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 17
US-08-865-579-22
; Sequence 22, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-865-579-22

Query Match 3.6%; Score 15; DB 4; Length 15;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 20
US-09-954-697-59
; Sequence 59, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697

;; CURRENT FILING DATE: 2001-09-14
;; NUMBER OF SEQ ID NOS: 116
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 59
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-954-697-59

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 20
US-09-257-218-6
; Sequence 6, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-6

Query Match 3.6%; Score 15; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 350 GFVSWRDPKSGSWYV 364
Db 32 GFVSWRDPKSGSWYV 46

RESULT 21

US-09-311-760-6
; Sequence 6, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
; FILING DATE: 13-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-311-760-6

Query Match 3.6%; Score 15; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 350 GFVSWRDPKSGSWYV 364
Db 32 GFVSWRDPKSGSWYV 46

RESULT 22
US-08-865-579-6
; Sequence 6, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

```

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; MOLECULE TYPE: peptide
; US-08-865-579-6
;
; Query Match 3.6%; Score 15; DB 4; Length 46;
; Best Local Similarity 100.0%; Pred. No. 5.6e-07; Indels 0; Gaps 0;
; Matches 15; Conservative 0; Mismatches 0;
;
QY 350 GFVSWRDPKSGSWYV 364
DB 32 GFVSWRDPKSGSWYV 46
;
; RESULT 23
; US-10-059-749-6
; Sequence 6, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; LITWACK, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
;
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
;
; MEDIUM TYPE: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-10-059-749-6
;
; Query Match 3.6%; Score 15; DB 4; Length 46;
; Best Local Similarity 100.0%; Pred. No. 5.6e-07; Indels 0; Gaps 0;
; Matches 15; Conservative 0; Mismatches 0;
;
QY 350 GFVSWRDPKSGSWYV 364
DB 32 GFVSWRDPKSGSWYV 46
;
; RESULT 24
; US-08-773-608A-2
; Sequence 2, Application US/08773608A
; Patent No. 5858778
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; LITWACK, Gerald
; TITLE OF INVENTION: Sf Caspase-1, Compositions and Methods
; TITLE OF INVENTION: for Making and Methods of Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5858778ris
; STREET: One Liberty Place 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: US
; ZIP: 19355
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,608A
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-773-608A-2
;
; Query Match 2.6%; Score 11; DB 2; Length 299;
; Best Local Similarity 100.0%; Pred. No. 0.021; Indels 0; Gaps 0;
; Matches 11; Conservative 0; Mismatches 0;
;
QY 277 GKPKLFFIQAC 287
DB 168 GKPKLFFIQAC 178
;
; RESULT 25
; US-09-187-789-38
; Sequence 38, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

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; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-38

Query Match          2.4%; Score 10; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPKLFFFIQAC 287
Db      21 KPKLFFFIQAC 30
|||||

RESULT 26
US-09-139-600-33
; Sequence 33, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-33

Query Match          2.4%; Score 10; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPKLFFFIQAC 287
Db      21 KPKLFFFIQAC 30
|||||

RESULT 27
US-08-462-969B-2
; Sequence 2, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,969B
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; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/334,251
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF140P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-969B-2

Query Match          2.4%; Score 10; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPKLFFFIQAC 287
Db      177 KPKLFFFIQAC 186
|||||

RESULT 28
US-09-561-756-24
; Sequence 24, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-24

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPKLFFFIQAC 287
Db      177 KPKLFFFIQAC 186
|||||

RESULT 29
US-09-227-721-24
; Sequence 24, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-24

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 30
US-09-556-627A-2
; Sequence 2, Application US/08556627A
; Patent No. 6462175
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,627A
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1813
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-556-627A-2

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 31
US-09-124-934A-2
; Sequence 2, Application US/09124934A
; Patent No. 6495519
; GENERAL INFORMATION:
```

```
; APPLICANT: He, Wei-Wu et al.,
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 a
; FILE REFERENCE: PF140C1
; CURRENT APPLICATION NUMBER: US/09/124,934A
; CURRENT FILING DATE: 1994-11-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-124-934A-2

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 32
US-08-724-378D-4
; Sequence 4, Application US/08724378D
; Patent No. 6512104
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; FILE REFERENCE: 06843-0019-00000
; CURRENT APPLICATION NUMBER: US/08/724,378D
; CURRENT FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-724-378D-4

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 33
US-08-334-251D-2
; Sequence 2, Application US/08334251D
; Patent No. 6538121
; GENERAL INFORMATION:
; APPLICANT: He et al.,
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 a
; FILE REFERENCE: PF140
; CURRENT APPLICATION NUMBER: US/08/334,251D
; CURRENT FILING DATE: 1994-11-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-334-251D-2

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 278 KPKLFFFIQAC 287
| | | | | | | |
Db 177 KPKLFFFIQAC 186

RESULT 34
US-09-954-697-24
; Sequence 24, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-24

Query Match 2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | |
Db 177 KPKLFFFIQAC 186

RESULT 35
US-09-163-099-2
; Sequence 2, Application US/09163099
; Patent No. 6686459
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch3, A No. 6686459el Apoptotic Protease,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/163,099
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/556,627
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1813
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

QY 278 KPKLFFFIQAC 287
| | | | | | | |
Db 177 KPKLFFFIQAC 186

RESULT 36
US-08-618-408B-2
; Sequence 2, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic
; TITLE OF INVENTION: Proteases, Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-618-408B-2

Query Match 2.4%; Score 10; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | |
Db 216 KPKLFFFIQAC 225

RESULT 37
US-08-724-378D-2
; Sequence 2, Application US/08724378D
```

```
; Patent No. 6512104
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-00000
; CURRENT APPLICATION NUMBER: US/08/724,378D
; CURRENT FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-724-378D-2

Query Match      2.4%; Score 10; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.25; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy      278 KPCLFFFIQAC 287
Db      259 KPCLFFFIQAC 268
|||||

RESULT 38
US-08-724-378D-3
; Sequence 3, Application US/08724378D
; Patent No. 6512104
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-00000
; CURRENT APPLICATION NUMBER: US/08/724,378D
; CURRENT FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-724-378D-3

Query Match      2.4%; Score 10; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.25; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy      278 KPCLFFFIQAC 287
Db      259 KPCLFFFIQAC 268
|||||

RESULT 39
US-08-665-220-2
; Sequence 2, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
```

```
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-220-2

Query Match      2.4%; Score 10; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy      278 KPCLFFFIQAC 287
Db      349 KPCLFFFIQAC 358
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RESULT 40
US-09-291-692-2
; Sequence 2, Application US/09291692
; Patent No. 6287795
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: Use
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,692
; FILING DATE: 04-13-1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-291-692-2

Query Match 2.4%; Score 10; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 41

US-09-561-756-33
Sequence 33, Application US/09561756
Patent No. 6376226
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431

CURRENT APPLICATION NUMBER: US/09/561.756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapien
US-09-561-756-33

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 42

US-09-227-721-33
Sequence 33, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapien
US-09-227-721-33

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 43

US-09-954-697-33
Sequence 33, Application US/09954697
Patent No. 6610541
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapien
US-09-954-697-33

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 44

US-09-009-893A-4
Sequence 4, Application US/09009893A
Patent No. 6623938
GENERAL INFORMATION:
APPLICANT: Ni, Jian

APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner L.
APPLICANT: Kenny, Joseph J.

TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/009,893A

CURRENT FILING DATE: 1998-02-21
PRIOR APPLICATION NUMBER: US 60/054,800
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/034,205
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-09-009-893A-4

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 45

US-09-489-155-4
Sequence 4, Application US/09489155
Patent No. 6680171

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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-834A-2
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
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DB 392 KPKLFFIQAC 401

RESULT 47
US-09-257-218-19
; Sequence 19, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-19

Query Match 2.2%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 FIQACGGEQ 291
| | | | | |
DB 1 FIQACGGEQ 9

RESULT 48
US-09-311-760-19
; Sequence 19, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa

```

```

1 Litack, Gerald
2
3 TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
4 Encoding same and Methods of Use
5
6 NUMBER OF SEQUENCES: 87
7
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Campbell & Flores LLP
10 STREET: 4370 La Jolla Village Drive, Suite 700
11 CITY: San Diego
12 STATE: California
13 COUNTRY: United States
14 ZIP: 92122
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/311,760
24 FILING DATE: 13-May-1999
25 CLASSIFICATION: <Unknown>
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 08/965,579
29 FILING DATE: <Unknown>
30
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Campbell, Cathryn A.
33 REGISTRATION NUMBER: 31,815
34 REFERENCE/DOCKET NUMBER: P-ID 2180
35
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (619) 535-9001
38 TELEFAX: (619) 535-9849
39
40 INFORMATION FOR SEQ ID NO: 19:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 9 amino acids
43 TYPE: amino acid
44 TOPOLOGY: linear
45
46 MOLECULE TYPE: peptide
47
48 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
49 US-09-311-760-19

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Query Match 2.2%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	283	FIQACGGEQ	291
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RESULT 49
US-09-561-756-56
; Sequence 56, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-56

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Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      283  FIOACGGEQ 291
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Db      1  FIOACGGEQ 9
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RESULT 50
US-09-227-721-56
; Sequence 56, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THREEOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-56

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Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels

QY 283 FIQACGGEQ 291
Db 1 FIQACGGEQ 9

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Copyright (c) 1993 - 2004 CompuGen Ltd.
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(without alignments)
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
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13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*	14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*	15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
Result No.	Score	Match	Length	DB	ID		
1	219	52.6	416	9	US-09-954-697-30	Sequence 30, Appl	
2	219	52.6	416	13	US-10-068-569-1	Sequence 1, Appl	
3	195	46.9	416	10	US-09-851-873-102	Sequence 102, Appl	
4	195	46.9	416	12	US-09-746-731-2	Sequence 2, Appl	
5	195	46.9	416	13	US-10-059-749-2	Sequence 4, Appl	
6	195	46.9	416	14	US-10-141-618-4	Sequence 172, Appl	
7	127	30.5	266	15	US-10-116-275-172	Sequence 27, Appl	
8	93	22.4	93	13	US-10-014-269-27	Sequence 27, Appl	
9	93	22.4	93	13	US-10-002-974-27	Sequence 27, Appl	
10	93	22.4	93	14	US-10-314-506-27	Sequence 27, Appl	
11	69	16.6	159	12	US-10-424-599-174531	Sequence 26, Appl	
12	42	10.1	42	14	US-10-153-344-26	Sequence 18, Appl	
13	32	7.7	32	13	US-10-068-569-18	Sequence 22, Appl	
14	32	7.7	32	13	US-10-068-569-22	Sequence 16, Appl	
15	19	4.6	19	14	US-10-153-344-16	Sequence 16, Appl	

16	15	3.6	15	9	US-09-954-697-59	Sequence 59, Appl
17	15	3.6	15	12	US-09-746-731-22	Sequence 22, Appl
18	15	3.6	15	13	US-10-068-569-6	Sequence 6, Appl
19	15	3.6	15	13	US-10-068-569-11	Sequence 11, Appl
20	15	3.6	15	13	US-10-059-749-22	Sequence 22, Appl
21	15	3.6	15	14	US-10-174-105A-131	Sequence 131, App
22	15	3.6	15	14	US-10-174-105A-132	Sequence 132, App
23	15	3.6	15	14	US-10-174-105A-176	Sequence 176, App
24	15	3.6	15	14	US-10-197-634-7	Sequence 7, Appl
25	15	3.6	46	12	US-09-746-731-6	Sequence 6, Appl
26	15	3.6	46	13	US-10-059-749-6	Sequence 6, Appl
27	12	2.9	13	14	US-10-174-105A-133	Sequence 133, App
28	12	2.9	13	14	US-10-174-105A-134	Sequence 134, App
29	10	2.4	10	14	US-10-153-344-17	Sequence 17, Appl
30	10	2.4	39	9	US-09-989-903-38	Sequence 38, Appl
31	10	2.4	39	14	US-10-068-564-38	Sequence 38, Appl
32	10	2.4	163	9	US-08-864-761-47950	Sequence 47950, A
33	10	2.4	303	9	US-09-895-263-2	Sequence 2, Appl
34	10	2.4	303	9	US-09-944-851-2	Sequence 2, Appl
35	10	2.4	303	9	US-09-954-697-24	Sequence 24, Appl
36	10	2.4	303	10	US-09-851-873-100	Sequence 100, App
37	10	2.4	303	14	US-10-337-060-2	Sequence 2, Appl
38	10	2.4	303	14	US-10-280-670-4	Sequence 4, Appl
39	10	2.4	389	14	US-10-280-670-2	Sequence 2, Appl
40	10	2.4	389	14	US-10-280-670-3	Sequence 3, Appl
41	10	2.4	479	9	US-09-952-768-2	Sequence 2, Appl
42	10	2.4	479	9	US-09-954-697-33	Sequence 33, Appl
43	10	2.4	479	10	US-09-009-893-4	Sequence 4, Appl
44	10	2.4	479	12	US-10-668-955-2	Sequence 2, Appl
45	10	2.4	479	16	US-10-713-208-4	Sequence 4, Appl
46	10	2.4	521	9	US-09-962-834A-2	Sequence 2, Appl
47	10	2.4	521	10	US-09-851-873-103	Sequence 103, App
48	10	2.4	521	14	US-10-439-676-2	Sequence 2, Appl
49	10	2.4	571	9	US-09-410-194-21	Sequence 21, Appl
50	9	2.2	9	9	US-09-954-697-56	Sequence 56, Appl
51	9	2.2	9	12	US-09-746-731-19	Sequence 19, Appl
52	9	2.2	9	13	US-10-059-749-19	Sequence 19, Appl
53	9	2.2	370	15	US-10-369-493-5719	Sequence 5719, Ap
54	9	2.2	415	12	US-10-424-599-251893	Sequence 251893,
55	9	2.2	481	9	US-09-410-194-12	Sequence 12, Appl
56	9	2.2	481	9	US-10-005-921-2	Sequence 2, Appl
57	9	2.2	629	12	US-10-425-114-69157	Sequence 69157, A
58	9	2.2	1121	16	US-10-240-577-2	Sequence 2, Appl
59	9	2.2	1196	10	US-09-823-394-2	Sequence 2, Appl
60	9	2.2	1196	16	US-10-240-577-6	Sequence 6, Appl
61	9	2.2	129	12	US-10-424-599-251890	Sequence 251890,
62	8	1.9	167	16	US-10-437-963-139812	Sequence 139812,
63	8	1.9	372	12	US-10-282-122A-77032	Sequence 77032, A
64	8	1.9	411	16	US-10-437-963-193992	Sequence 193992,
65	8	1.9	579	14	US-10-080-170-242	Sequence 242, App
66	8	1.9	579	16	US-10-080-170-242	Sequence 242, App
67	8	1.9	752	15	US-10-369-493-5384	Sequence 5384, Ap
68	8	1.9	758	15	US-10-369-493-5369	Sequence 5369, Ap
69	8	1.9	764	16	US-10-437-963-111189	Sequence 111189,
70	8	1.9	794	15	US-10-369-493-5131	Sequence 5131, Ap
71	8	1.9	794	15	US-10-369-493-5132	Sequence 5132, Ap
72	8	1.9	1218	15	US-10-289-762-98	Sequence 98, Appl
73	8	1.9	1397	12	US-10-282-122A-54874	Sequence 54874, A
74	8	1.9	1397	9	US-09-965-967-12	Sequence 12, Appl
75	7	1.7	7			

ALIGNMENTS

RESULT 1
US-09-954-697-30
; Sequence 30, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Ebad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF

```

; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30

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Query Match	52.6%	Score 219;	DB 9;	Length 416;
Best Local Similarity	100.0%;	Pred. No. 1.7e-199;		
Matches 219;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	258	VSVSEKIVNIENGTSCPSLGGKPKLFFTOACGGEQKHGFVASTSPDESPGNSPEPDAT	317	
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QY	378	EDLQSLLLRVANASVVGKGYKQMPGCFNFKLFFKITS	416	
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RESULT 2
US-10-068-569-1
; Sequence 1, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-1

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	Query Match	52.6%;	Score 219;	DB 13;	Length 416;
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Db	97	KLSKPTLENLTPVULR	PEIRKEVILRPTPR	PVDIGSGGFGDVG	ALSLRGNADLAYILS 156
Qy	157	MEPCGHCLIIINNVN	FCRSGGLTRTGSNI	DCBKLRRRFSLLHF	MEVVEVGDLTAKQWIAL 216
Db	157	MEPCGHCLIIINNVN	FCRSGGLTRTGSNI	DCBKLRRRFSLLHF	MEVVEVGDLTAKQWIAL 216
Qy	217	LELARQDHGALDCCVV	VILSHGCSQASHLQF	PGAVYGTGDCPVS	VEKIVNIENGTSCPSLG 276
Db	217	LELARQDHGALDCCVV	VILSHGCSQASHLQF	PGAVYGTGDCPVS	VEKIVNIENGTSCPSLG 276
Qy	277	GKPKLFFTOACGGE	QKHGFVEVASTS	PEDESFGSNPEPDAT	PFQEGRTFDQLDAISLPP 336
Db	277	GKPKLFFTOACGGE	QKHGFVEVASTS	PEDESFGSNPEPDAT	PFQEGRTFDQLDAISLPP 336

Qy	337	TPSDIIVFSYSTFGFVSWRDPKGSWVETLDDIFEQWASEDLQSLLLRVANASVKGI	396
Db	337	TPSDIIVFSYSTFGFVSWRDPKGSWVETLDDIFEQWASEDLQSLLLRVANASVKGI	396
Qy	397	YKMPGCGFNLRKLLFPKTS	416
Db	397	YKMPGCGFNLRKLLFPKTS	416

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RESULT 3
US-09-851-873-102
; Sequence 102, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851.873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-102

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Query Match	46.9%;	Score 195;	DB 10;	Length 416;
Best Local Similarity	100.0%;	Pred. NO. 1.2e-176;		
Matches 195;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	222	QDHGALDCCVVVILSHGCGQASHLOFP	PGGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL	281
Db	222	QDHGALDCCVVVILSHGCGQASHLOFP	PGGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL	281
Qy	282	FFIQACGGEQKHGDFEAVASTP	DEBSPGNSNPEDATPQEGRLTFDQLDAISLPPPSDI	341
Db	282	FFIQACGGEQKHGDFEAVASTP	DEBSPGNSNPEDATPQEGRLTFDQLDAISLPPPSDI	341
Qy	342	FVSYSTPFGVSWRDPKSGSWMVETLDDI	FEQWAHSEDLQSLLLRVANAVSVKGIYKQMP	401
Db	342	FVSYSTPFGVSWRDPKSGSWMVETLDDI	FEQWAHSEDLQSLLLRVANAVSVKGIYKQMP	401
Qy	402	GCNFRLRKKLFFKTS	416	
Db	402	GCNFRLRKKLFFKTS	416	

RESULT 4
US-09-746-731-2
Sequence 2, Application US/09746731
Publication No. US20010016345A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Bernardes-Alnemri, Teresa
Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mcb6, Nucleic Acids
Containing Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-746-731-2

Query Match          46.9%; Score 195; DB 12; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKDHGFVASTSPEDSPGSPNPEPATPFQGLRTFDQLDAISSLPTPSDI 341
Db 282 FFIQACGGEQKDHGFVASTSPEDSPGSPNPEPATPFQGLRTFDQLDAISSLPTPSDI 341
QY 342 FVSYSTPFGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
Db 342 FVSYSTPFGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
QY 402 GCFNFKLKKLFKTS 416
Db 402 GCFNFKLKKLFKTS 416

RESULT 5
US-10-059-749-2
; Sequence 2, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
;               Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579

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;
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match          46.9%; Score 195; DB 13; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKDHGFVASTSPEDSPGSPNPEPATPFQGLRTFDQLDAISSLPTPSDI 341
Db 282 FFIQACGGEQKDHGFVASTSPEDSPGSPNPEPATPFQGLRTFDQLDAISSLPTPSDI 341
QY 342 FVSYSTPFGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
Db 342 FVSYSTPFGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
QY 402 GCFNFKLKKLFKTS 416
Db 402 GCFNFKLKKLFKTS 416

```

```

RESULT 6
US-10-141-618-4
; Sequence 4, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; FILE OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-618-4

Query Match          46.9%; Score 195; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKDHGFVASTSPEDSPGSPNPEPATPFQGLRTFDQLDAISSLPTPSDI 341

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Db 282 FFIQACGGEQKHGFVAVSTSPEDSPGSGNPEPDATPFQGLRTFDQLDAISSLPTSDI 341
Qy 342 FVSYSTPPGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMP 401
Db 342 FVSYSTPPGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMP 401
Qy 402 GCFNFKLKKLFFKTS 416
Db 402 GCFNFKLKKLFFKTS 416

RESULT 7
US-10-116-275-172
; Sequence 172, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'hahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-172

Query Match 30.5%; Score 127; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 4e-112;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 EQKHGFVAVSTSPEDSPGSGNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPP 349
Db 140 EQKHGFVAVSTSPEDSPGSGNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPP 199
Qy 350 GFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMPGCCFNFLK 409
Db 200 GFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMPGCCFNFLK 259
Qy 410 KLFKTS 416
Db 260 KLFKTS 266

RESULT 8
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT APPLICATION NUMBER: US/10/014,269
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27

Query Match 22.4%; Score 93; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLVBEQLQDVLVLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLVBEQLQDVLVLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 9
US-10-002-974-27
; Sequence 27, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-974-27

Query Match 22.4%; Score 93; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLVBEQLQDVLVLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLVBEQLQDVLVLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 10
US-10-314-506-27
; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,269
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,289
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-506-27

Query Match 22.4%; Score 93; DB 14; Length 93;

Db 282 FFIQACGGEQKHGFVAVSTSPEDSPGSGNPEPDATPFQGLRTFDQLDAISSLPTSDI 341
Qy 342 FVSYSTPPGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMP 401
Db 342 FVSYSTPPGFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMP 401
Qy 402 GCFNFKLKKLFFKTS 416
Db 402 GCFNFKLKKLFFKTS 416

RESULT 7
US-10-116-275-172
; Sequence 172, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'hahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-172

Query Match 30.5%; Score 127; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 4e-112;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 EQKHGFVAVSTSPEDSPGSGNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPP 349
Db 140 EQKHGFVAVSTSPEDSPGSGNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPP 199
Qy 350 GFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMPGCCFNFLK 409
Db 200 GFVSWRDPKSGWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMPGCCFNFLK 259
Qy 410 KLFKTS 416
Db 260 KLFKTS 266

RESULT 8
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT APPLICATION NUMBER: US/10/014,269
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27

Query Match 22.4%; Score 93; DB 13; Length 93;

Best Local Similarity 100.0%; Pred. No. 3.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

Qy 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 11
US-10-424-599-174531
; Sequence 174531, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174531
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12861C.1.pep
US-10-424-599-174531

Query Match 16.6%; Score 69; DB 12; Length 159;
Best Local Similarity 100.0%; Pred. No. 3.9e-57;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CRLRLVEELQVQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLIIDLETRGSQALP 71
Db 12 CRLRLVEELQVQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLIIDLETRGSQALP 71

Qy 72 LFISCLEDT 80
Db 72 LFISCLEDT 80

RESULT 12
US-10-153-344-26
; Sequence 26, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 26
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-153-344-26

Query Match 10.1%; Score 42; DB 14; Length 42;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 GSGSRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASF 88
Db 1 GSGSRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASF 42

RESULT 13
US-10-068-569-18
; Sequence 18, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 18
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-18

Query Match 7.7%; Score 32; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 PEDESPGSNPEPDATPFQEGSLRTFDQDAISS 334
Db 1 PEDESPGSNPEPDATPFQEGSLRTFDQDAISS 32

RESULT 14
US-10-068-569-22
; Sequence 22, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-22

Query Match 7.7%; Score 32; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 PEDESPGSNPEPDATPFQEGSLRTFDQDAISS 334
Db 1 PEDESPGSNPEPDATPFQEGSLRTFDQDAISS 32

RESULT 15
US-10-153-344-16
; Sequence 16, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM

```
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; PRIOR FILING DATE: 2002-08-27
; PRIORITY APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-153-344-16

Query Match      4.6%; Score 19; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 WDVLLSRLPRPHMIEDIQ 44
Db 1 WDVLLSRLPRPHMIEDIQ 19

RESULT 16
US-09-954-697-59
; Sequence 59, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-954-697-59

Query Match      3.6%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 17
US-09-746-731-22
; Sequence 22, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
;               Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; PRIOR FILING DATE: 2002-08-27
; PRIORITY APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: PC-DOS/MS-DOS
; US-09-961-201a-1.oligo.rapb

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,731
FILING DATE: 22-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-746-731-22

Query Match      3.6%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 18
US-10-068-569-6
; Sequence 6, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-068-569-6

Query Match      3.6%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 ATPFOEGLRTFDQLD 330
Db 1 ATPFOEGLRTFDQLD 15

RESULT 19
US-10-068-569-11
; Sequence 11, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
```

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; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-11

Query Match          3.6%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFQGLRTFDQLD 330
Db 1 ATPFQGLRTFDQLD 15

RESULT 20
US-10-059-749-22
; Sequence 22, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-059-749-22

Query Match          3.6%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 21
US-10-174-105A-131
; Sequence 131, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD RES
; LOCATION: {10}..(10)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-131

Query Match          3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CEKLRRRFSSSLHFMV 201
Db 1 CEKLRRRFSSSLHFMV 15

RESULT 22
US-10-174-105A-132
; Sequence 132, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-174-105A-132

Query Match          3.6%; Score 15; DB 14; Length 15;
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Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CEKLRFRFSSLHFVW 201
Db 1 CEKLRFRFSSLHFVW 15

RESULT 23
US-10-174-105A-176
; Sequence 176, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-176

Query Match 3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CEKLRFRFSSLHFVW 201
Db 1 CEKLRFRFSSLHFVW 15

RESULT 24
US-10-197-634-7
; Sequence 7, Application US/10197634
; Publication No. US20030073629A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
; FILE REFERENCE: 480140.479
; CURRENT APPLICATION NUMBER: US/10/197,634
; CURRENT FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-634-7

Query Match 3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFQGLRTFDQD 330

Db 1 ATPFQGLRTFDQD 15

RESULT 25
US-09-746-731-6
; Sequence 6, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-3849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-746-731-6

Query Match 3.6%; Score 15; DB 12; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 32 GFVSWRDPKSGSWYV 46

RESULT 26
US-10-059-749-6
; Sequence 6, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700


```
/ STREET: 9410 Key West Ave.
/ CITY: Rockville
/ STATE: MD
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/895.263
/ FILING DATE: 02-Jul-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: <Unknown>
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jonathan L. Klein
/ REGISTRATION NUMBER: 41,119
/ REFERENCE/DOCKET NUMBER: PF140
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 301-251-6015
/ TELEFAX: 301-309-8439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-895-263-2

Query Match 2.4%; Score 10; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 177 KPKLFFIQAC 186

RESULT 34
US-09-944-851-2
/ Sequence 2, Application US/09944851
/ Patent No. US20020102648A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/944,851
/ FILING DATE: 31-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/556,627
/ FILING DATE: 13-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-ID 1813
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-851-2

Query Match 2.4%; Score 10; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 177 KPKLFFIQAC 186

RESULT 35
US-09-954-697-24
/ Sequence 24, Application US/09954697
/ Patent No. US20020106631A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
/ FILE REFERENCE: 480140.431D2
/ CURRENT APPLICATION NUMBER: US/09/954,697
/ CURRENT FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 24
/ LENGTH: 303
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-954-697-24

Query Match 2.4%; Score 10; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 177 KPKLFFIQAC 186

RESULT 36
US-09-851-873-100
/ Sequence 100, Application US/09851873
/ Publication No. US20030165488A1
/ GENERAL INFORMATION:
/ APPLICANT: Kletzien, Rolf F
/ APPLICANT: Reardon, Ilene M
/ APPLICANT: Weiland, Katherine L
/ TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
/ FILE REFERENCE: 28341/00233
/ CURRENT APPLICATION NUMBER: US/09/851,873
/ CURRENT FILING DATE: 2001-05-08
/ NUMBER OF SEQ ID NOS: 105
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 100
/ LENGTH: 303
/ TYPE: PRT
/ ORGANISM: Homo sapiens
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US-09-851-873-100

Query Match 2.4%; Score 10; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 177 KPCLFFFIQAC 186

RESULT 37

US-10-337-060-2
; Sequence 2, Application US/10337060
; Publication No. US20030119169A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH3, A NOVEL APOPTOTIC PROTEASE,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; FILE REFERENCE: 480140.423D2
; CURRENT APPLICATION NUMBER: US/10/337,060
; CURRENT FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-060-2

Query Match 2.4%; Score 10; DB 14; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 177 KPCLFFFIQAC 186

RESULT 38

US-10-280-670-4
; Sequence 4, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-4

Query Match 2.4%; Score 10; DB 14; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 177 KPCLFFFIQAC 186

RESULT 39

US-10-280-670-2
; Sequence 2, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-2

Query Match 2.4%; Score 10; DB 14; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 259 KPCLFFFIQAC 268

RESULT 40

US-10-280-670-3
; Sequence 3, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-3

Query Match 2.4%; Score 10; DB 14; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 259 KPCLFFFIQAC 268

RESULT 41

US-09-952-768-2
; Sequence 2, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; ; Fernandes-Alnemri, Teresa

```
/ Litwack, Gerald
/ Armstrong, Robert
/ Tomaselli, Kevin
/
/ TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
/ NUCLEIC ACIDS ENCODING AND METHODS OF USE
/
/ NUMBER OF SEQUENCES: 75
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seed Intellectual Property Law Group
/ STREET: Suite 6300, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/952,768
/ FILING DATE: 10-Sep-2001
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Christiansen, William T.
/ REGISTRATION NUMBER: 44,614
/ REFERENCE/DOCKET NUMBER: 480140.424C4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 692-6031
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 479 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-952-768-2

Query Match 2.4%; Score 10; DB 9; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 349 KPKLFFIQAC 358

RESULT 42
US-09-954-697-33
/ Sequence 33, Application US/09954697
/ Patent No. US20020106631A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 480140.431D2
/ CURRENT APPLICATION NUMBER: US/09/954,697
/ CURRENT FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 33
/ LENGTH: 479
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-954-697-33

Query Match 2.4%; Score 10; DB 9; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 349 KPKLFFIQAC 358
```

```
RESULT 43
US-09-009-893-4
/ Sequence 4, Application US/09009893
/ Publication No. US20030087339A1
/ GENERAL INFORMATION:
/ APPLICANT: NI, JIAN
/ APPLICANT: ROSEN, CRAIG A.
/ APPLICANT: DIXIT, VISHVA M.
/ APPLICANT: GENTZ, REINER L.
/ APPLICANT: KENNY, JOSEPH J.
/ TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
/ NUMBER OF SEQUENCES: 32
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
/ STREET: 1100 NEW YORK AVENUE, SUITE 600
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: US
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/009,893
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/034,205
/ FILING DATE: 21-JAN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/054,800
/ FILING DATE: 05-AUG-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: STEFFE, ERIC K.
/ REGISTRATION NUMBER: 36,688
/ REFERENCE/DOCKET NUMBER: 1488.0970002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 479 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-009-893-4
```

```
Query Match 2.4%; Score 10; DB 10; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 278 KPKLFFIQAC 287
Db 349 KPKLFFIQAC 358
```

```
RESULT 44
US-10-668-955-2
/ Sequence 2, Application US/10668955
/ Publication No. US20040054148A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Fernandes-Alnemri, Teresa
/ Litwack, Gerald
/ Armstrong, Robert
/ Tomaselli, Kevin
/ TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
```

NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/668,955
FILING DATE: 22-Sep-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Laherty, Carol D.
REGISTRATION NUMBER: 51,909
REFERENCE/DOCKET NUMBER: 480140.424D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-668-955-2

Query Match 2.4%; Score 10; DB 12; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | | | |
Db 349 KPKLFFFIQAC 358

RESULT 45
US-10-713-208-4
; Sequence 4, Application US/10713208
; Publication No. US20040121387A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
; TITLE OF INVENTION: CD-95 Induced Apoptosis
; FILE REFERENCE: PF381C1D1
; CURRENT APPLICATION NUMBER: US/10/713,208
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 09/489,155
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-208-4

Query Match 2.4%; Score 10; DB 16; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | | | |
Db 349 KPKLFFFIQAC 358
RESULT 46
US-09-962-834A-2
; Sequence 2, Application US/09962834A
; Patent No. US20020034813A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: NOVEL PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,834A
; FILING DATE: 25-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 08/675,123
; FILING DATE: 1996-07-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-834A-2

Query Match 2.4%; Score 10; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | | | |
Db 392 KPKLFFFIQAC 401

RESULT 47
US-09-851-873-103
; Sequence 103, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 103
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-103

Query Match 2.4%; Score 10; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 392 KPXLFFFIQAC 401
|||||

RESULT 48

US-10-439-676-2
; Sequence 2, Application US/10439676
; Publication No. US20030180935A1
; GENERAL INFORMATION:

; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: NOVEL PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/439,676

; FILING DATE: 16-May-2003

; CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/675,123

; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; REFERENCE/DOCKET NUMBER: G15276

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 521 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-439-676-2

Query Match 2.4%; Score 10; DB 14; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 392 KPXLFFFIQAC 401
|||||

RESULT 49

US-09-410-194-21

; Sequence 21, Application US/09410194

; Patent No. US20020095030A1

; GENERAL INFORMATION:

; APPLICANT: Tschoopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-21

Query Match 2.4%; Score 10; DB 9; Length 571;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 392 KPXLFFFIQAC 401
|||||

RESULT 50

US-09-954-697-56

; Sequence 56, Application US/09954697

; Patent No. US20020108631A1

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSSES

; FILE REFERENCE: 480140.431D2

; CURRENT APPLICATION NUMBER: US/09/954,697

; CURRENT FILING DATE: 2001-09-14

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 56

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-954-697-56

Query Match 2.2%; Score 9; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 FIQACGGEG 291
Db 1 FIQACGGEG 9
|||||

Search completed: August 3, 2004, 09:16:26
Job time : 46 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2004, 09:03:12 ; Search time 55 Seconds
(without alignments)
2137.087 Million cell updates/sec

Title: US-09-961-201A-1
Perfect score: 416
Sequence: 1 MDEADRLRLRCLRLVEEL.....YKQMGCFNLRKKUFFKTS 416

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	416	100.0	416	2	Aaw39209 Human ICE
2	416	100.0	416	4	Aae00606 Human cas
3	219	52.6	416	2	Aay21723 Amino aci
4	219	52.6	416	5	Abj01224 Human cas
5	219	52.6	416	6	Ada10646 Human cas
6	202	48.6	203	2	Aaw39208 Human ICE
7	195	46.9	416	4	Aag67375 Amino aci
8	195	46.9	416	4	Aau08315 Human asp
9	195	46.9	416	4	Aae08938 Mammalian
10	195	46.9	416	4	Aab84374 Amino aci
11	195	46.9	416	6	Abb82738 Human cas
12	195	46.9	416	8	Ades2020 Human mam
13	127	30.5	266	4	Aae00620 Human cas
14	124	29.8	401	6	Ada10677 Human cas
15	124	29.8	416	6	Ada10675 Human cas
16	124	29.8	416	6	Ada10676 Human cas
17	124	29.8	416	6	Ada10674 Human cas
18	93	22.4	93	5	Abj04760 Caspase-9
19	42	10.1	42	6	Abp71130 Mch6 CARD
20	32	7.7	32	6	Ada10663 Human pro
21	32	7.7	32	6	Ada10667 Human pro
22	19	4.6	19	6	Abp71113 Mch6 prot
23	15	3.6	15	2	Aay21739 Conserved
24	15	3.6	15	4	Aae08955 Mammalian
25	15	3.6	15	5	Abj01243 Human cas

ALIGNMENTS

RESULT 1
AAW39209
ID AAW39209 standard; peptide; 416 AA.

AC AAW39209;

DT 18-MAY-1998 (first entry)

DE Human ICE LAP-6 polypeptide.

KW ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;

KW viral infection; tumour; inflammation; osteoporosis; AIDS; human;

XX Alzheimer's disease.

OS Homo sapiens.

XX EP0808904-A2.

PN

26	15	3.6	15	6	ABP71313	Abp71313 Human cas
27	15	3.6	15	6	ADA10656	Ada10656 Mouse cas
28	15	3.6	15	6	ADA10651	Ada10651 Human cas
29	15	3.6	46	4	AAE08939	Aae08939 Mammalian
30	15	3.6	46	8	ADE52024	Ades2024 Aspartate
31	14	3.4	14	4	AAW97045	Aaw97045 Human pep
32	12	2.9	15	4	AAU08321	Aau08321 Human MCH
33	11	2.6	299	2	AAW89198	Aaw89198 Aspartate
34	11	2.6	323	4	ABB61468	Abb61468 Drosophil
35	11	2.6	339	4	ABB58379	Abb58379 Drosophil
36	10	2.4	10	6	ABP71122	Abp71122 Mch6 prot
37	10	2.4	163	4	AAW68529	Aaw68529 Human bon
38	10	2.4	163	5	ABG38107	Abg38107 Human pep
39	10	2.4	244	4	AAW98655	Aaw98655 Caspase-7
40	10	2.4	303	2	AAW15262	Aaw15262 Apototic
41	10	2.4	303	2	AAW15247	Aaw15247 Cysteine
42	10	2.4	303	2	AAW21721	Aay21721 Amino aci
43	10	2.4	303	4	AAE00604	Aae00604 Human cas
44	10	2.4	303	5	ABJ01222	Abj01222 Human cas
45	10	2.4	303	5	ABB78588	Abb78588 Mouse cas
46	10	2.4	303	5	ABB09299	Abb09299 Human cas
47	10	2.4	303	5	ABB09297	Abb09297 Human cas
48	10	2.4	303	6	AAO19868	Aao19868 Bacteriop
49	10	2.4	308	4	ABB69920	Abb69920 Drosophil
50	10	2.4	336	5	ABB09300	Abb09300 Human cas
51	10	2.4	340	5	ABB09298	Abb09298 Mouse cas
52	10	2.4	341	2	AAW95830	Aaw95830 Human int
53	10	2.4	389	2	AAW54392	Aaw54392 Human LIC
54	10	2.4	479	2	AAW27390	Aaw27390 Mch4 prot
55	10	2.4	479	2	AAW76629	Aaw76629 Human Mch
56	10	2.4	479	2	AAW21724	Aay21724 Amino aci
57	10	2.4	479	4	AAE00621	Aae00621 Human cas
58	10	2.4	479	5	ABJ01225	Abj01225 Human cas
59	10	2.4	479	7	ADA10617	Ada10617 Human Mch
60	10	2.4	521	2	AAW50007	Aaw50007 Human pro
61	10	2.4	521	4	AAE00607	Aae00607 Human cas
62	9	2.2	9	2	AAW21736	Aay21736 Conserved
63	9	2.2	9	4	AAU08318	Aau08318 Human MCH
64	9	2.2	9	4	AAE08952	Aae08952 Mammalian
65	9	2.2	9	5	ABJ01240	Abj01240 Human cas
66	9	2.2	9	6	AAE35831	Aae35831 hCasp-9 N
67	9	2.2	481	2	AAW76632	Aaw76632 Mouse CFL
68	9	2.2	481	3	AAE03958	Aae03958 FLICE-lik
69	9	2.2	481	5	ABB09295	Abb09295 Mouse FLI
70	9	2.2	483	2	AAW76626	Aaw76626 Murine FL
71	9	2.2	484	5	ABB09292	Abb09292 Mouse FLI
72	9	2.2	484	6	ABB99383	Abb99383 Amino aci
73	9	2.2	1121	4	AAW79244	Aaw79244 Amino aci
74	9	2.2	1164	5	ABB92294	Abb92294 Herbicida
75	9	2.2	1196	2	AAW97819	Aaw97819 Arabidops

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PD 26-NOV-1997.
XX
PF 19-MAY-1997; 97EP-00303397.
XX
PR 20-MAY-1996; 96US-0017949P.
PR 23-MAY-1996; 96US-0020344P.
PR 05-JUN-1996; 96US-0018961P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI ) UNIV MICHIGAN.
XX
PI Dixit VM, He W, Ruben SM, Kikly KK;
XX
DR WPI; 1998-001790/01.
DR N-PSDB; AAV09401.
XX
PT DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -
PT useful to develop products to treat, e.g. viral infection, tumour,
PT Alzheimer's disease, inflammation, osteoporosis and AIDS.
XX
PS Claim 4; Fig 1; 44pp; English.
XX
CC This is a human interleukin-1 beta converting enzyme apoptosis protease-6
CC (ICE LAP-6) polypeptide. The ICE LAP-6 polypeptide and agonists to the
CC polypeptide can be used to induce apoptosis, e.g. as an antiviral or
CC antitumour agent, control embryonic development and tissue homeostasis
CC and the roles of such factors in dysfunction and disease. Antagonists
CC which inhibit the activity of the ICE LAP-6 polypeptide can be used to
CC treat, Alzheimer's or Parkinson's disease, rheumatoid arthritis, septic
CC shock, sepsis, stroke, chronic, acute or central nervous system
CC inflammation, osteoporosis, ischaemia reperfusion injury, cell death
CC associated with cardiovascular disease, polycystic kidney disease,
CC apoptosis of endothelial cells in cardiovascular disease, degenerative
CC liver disease, multiple sclerosis, cerebellar degeneration, ischaemic
CC injury, myocardial infarction, acquired immunodeficiency syndrome (AIDS),
CC myelodysplastic syndrome, aplastic anaemia, male pattern baldness and
CC head injury damage. They can also be used for detection and diagnosis
XX
SQ Sequence 416 AA;
Query Match 100.0%; Score 416; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDEADRLRLRCRLRVLEELQVDQLWVLLSRELFPRHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRVLEELQVDQLWVLLSRELFPRHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSAQLPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120
Db 61 DLETRGSAQLPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120
Qy 121 LRPTPRVDITGSGGFGDVGALSLRGADLALAYILSMPECGHCLIIINNFCRESGLRTR 180
Db 121 LRPTPRVDITGSGGFGDVGALSLRGADLALAYILSMPECGHCLIIINNFCRESGLRTR 180
Qy 181 TGSNIDCKLRRRSSLHFVVEVKGDLTAKKMWLALLEELARQDHGALDCCVVLISHGQC 240
Db 181 TGSNIDCKLRRRSSLHFVVEVKGDLTAKKMWLALLEELARQDHGALDCCVVLISHGQC 240
Qy 241 ASHLQFPQAVYGTGCPVSVKIVNIENGTSKPSLGGKPKLFFTOACGGEOKDHGFVAS 300
Db 241 ASHLQFPQAVYGTGCPVSVKIVNIENGTSKPSLGGKPKLFFTOACGGEOKDHGFVAS 300
Qy 301 TSPDESPGSPNEPDATPFQGLRFTDQDLAISLPTPSDIFVSYSTPFGVSWRDPKSG 360
Db 301 TSPDESPGSPNEPDATPFQGLRFTDQDLAISLPTPSDIFVSYSTPFGVSWRDPKSG 360
Qy 361 SWYVETLDDIFEQWAHSEDQLSLLLRVANAVSVKGIYKQMPCCNFRLKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDQLSLLLRVANAVSVKGIYKQMPCCNFRLKLLFFKTS 416
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RESULT 2

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AAE00606
ID AAE00606 standard; protein; 416 AA.
XX
AC AAE00606;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human caspase-9, alternative version.
XX
KW Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6;
KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
KW tumour; cathepsin B; urokinase; proliferation; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 28
FT /note= "Encoded by GCC; Ala is present in the sequence
FT shown in page 105-107 (AAE00620)"
FT
FT Misc-difference 96
FT /note= "Encoded by GCA; Ala is present in the sequence
FT shown in page 105-107 (AAE00620)"
FT
FT Misc-difference 139..290
FT /note= "Encoded by GTCGAG; Amino acid residues from
FT position 140 to 289 present in this sequence are not
FT found in the sequence shown in page 105-107 (AAE00620)"
FT
FT Cleavage-site 315..316
FT /label= Proteolytic_cleavage_site
FT
FT Cleavage-site 330..331
FT /label= Proteolytic_cleavage_site
XX
XX WO200129232-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-US028941.
XX
XX 20-OCT-1999; 99US-0160559P.
XX
XX 14-AUG-2000; 2000US-0225564P.
XX
XX (SCIO-) SCIOS INC.
XX
XX Cordell B, Li Y;
XX
XX WPI; 2001-290920/30.
XX
XX N-PSDB; AAD03916.
XX
XX Novel fusion polypeptide comprising first and second caspase subunit
XX separated by cleavage site not associated in nature with caspase subunit,
XX useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage.
XX
XX Claim 4; Fig 18; 116pp; English.
XX
XX The present sequence is an alternative version of human Caspase-9 also
XX known as interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases
XX are a family of cysteine proteases, that participate in the initiation
XX and execution of apoptosis. Caspases exist as pro-enzymes, activated by
XX cleavage into a large and small subunit, occurring after specific
XX aspartic acid residues within the pro-enzyme sequence. The present
XX invention relates to a method for functional cloning of genes encoding
XX proteins or enzymes involved in proteolytic cleavage. The invention is
XX based on the use of caspase expression cassettes comprising the coding
XX sequence of a proteolytic cleavage site flanked by sequences encoding two
XX caspase subunits. A fusion polypeptide comprising a first and a second
XX caspase subunit, separated by a cleavage site not associated in nature,
XX is useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage. An expression cassette containing fusion polypeptide is used to
XX identify a mutant cell line deficient in an enzyme of interest and is
XX also useful for diagnosis and suppression of proliferation or metastases
XX of a tumour cell characterised by overexpression of a polypeptide (e.g.
```


CC Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
CC encoding fusion polypeptide is used in gene therapy. Note: This sequence
CC SEQ.ID.NO.18 is stated as being the same as that shown in page 105-107
CC (See AAB00620) in the specification. However these sequences differ at
CC several positions
XX
XX Sequence 416 AA;
S
Query Match 100.0%; Score 416; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCKRLRVELOVDQLDWVLLSRLFRPHMEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCKRLRVELOVDQLDWVLLSRLFRPHMEDIQAGSGSRDDQARQLII 60
QY 61 DLETGSQLPLFISLEDTGDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETGSQLPLFISLEDTGDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETPRVDIGSGGPDVGALESRLGNADLAYILSMPCGHCLIIINNVNFCRESGLRTR 180
Db 121 LRPETPRVDIGSGGPDVGALESRLGNADLAYILSMPCGHCLIIINNVNFCRESGLRTR 180
QY 181 TGSNDCEKLRREFSLHFWVEKGLDTAKKMWLALLELARQDHGALDCVVLVILSHGCG 240
Db 181 TGSNDCEKLRREFSLHFWVEKGLDTAKKMWLALLELARQDHGALDCVVLVILSHGCG 240
QY 241 ASHLOPPGAVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLOPPGAVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPEDSPGSGNPEPDATPQEGRLRTDQLDAISSLTPSDIFVSYSTFPFVSWRDPKSG 360
Db 301 TSPEDSPGSGNPEPDATPQEGRLRTDQLDAISSLTPSDIFVSYSTFPFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDQLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDQLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416
RESULT 3
AAV21723
ID AAY21723 standard; protein; 416 AA.
AC AAY21723;
XX
XX 10-SEP-1999 (first entry)
XX
XX Amino acid sequence of caspase-9 (ICE-LAP6).
DE
XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW tumour cell; myocardial infarction; human.
XX
XX Homo sapiens.
XX WO9935277-A2.
FN
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-US000632.
PF
XX 09-JAN-1998; 98US-0070987P.
PR
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX WPI; 1999-419353/35.
DR N-PSDB; AAX81225.
XX
XX New isolated nucleic acid molecule encoding a rev-caspase - used for

PT screening and identifying inhibitors or enhancers for treating cancer or
PT autoimmune disease.
XX
XX Disclosure; Fig 19A-B; 7app; English.
XX
CC The invention relates to nucleic acid molecules encoding rev-caspases.
CC Rev-caspases are cysteine proteases that specifically cleave proteins
CC after Asp residues and is expressed as a zymogen, in which the small
CC subunit is N-terminal to a large subunit. A gene delivery vehicle
CC comprising a rev-caspase coding sequence is useful for the treatment of
CC cancer, where the gene delivery vehicle is internalised by tumour cells.
CC The gene delivery vehicle can also be used to treat autoimmune diseases.
CC Cells transfected with a rev-caspase expressing vector can be used in
CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
CC In vitro translated rev-caspase can be used to identify an inhibitor or
CC enhancer of caspase processing activity. Caspase inhibitors are useful
CC for treating neurodegenerative diseases as well as for inhibiting
CC apoptosis in the heart following myocardial infarction. Sequences
CC AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
CC gene products (AAY21715-Y21724)
XX
XX Sequence 416 AA;
S
Query Match 52.6%; Score 219; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.3e-208;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 HFVMEVKGDLTAKKMWLALLELARQDHGALDCVVLVILSHGCOASHLOPPGAVYGTGCP 257
Db 198 HFVMEVKGDLTAKKMWLALLELARQDHGALDCVVLVILSHGCOASHLOPPGAVYGTGCP 257
QY 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDSPGSGNPEPDAT 317
Db 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDSPGSGNPEPDAT 317
QY 318 PQEGLRTFDQLDAISSLTPSDIFVSYSTFPFVSWRDPKSGWYVETLDDIFEQWAHS 377
Db 318 PQEGLRTFDQLDAISSLTPSDIFVSYSTFPFVSWRDPKSGWYVETLDDIFEQWAHS 377
QY 378 EDLQSLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416
Db 378 EDLQSLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416
RESULT 4
ABJ01224
ID ABJ01224 standard; protein; 416 AA.
XX
XX AC ABJ01224;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human caspase-9 SEQ ID NO: 30.
DE
XX
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
KW autoimmune disease; cytostatic; immunosuppressive.
XX
XX Homo sapiens.
XX OS
XX US6376226-B1.
FN
XX 23-APR-2002.
PD
XX 26-APR-2000; 2000US-00561756.
PF
XX 09-JAN-1998; 98US-0070897P.
PR
XX 08-JAN-1999; 99US-00227721.
PR
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX WPI; 2002-453146/48.
DR

DR N-PSDB; ABT03972.
XX
XX New rev-caspases engineered to contain the small subunit fused in frame N
PT -terminal to the large subunit, which is in reverse order to the wild
PT type caspases, are useful to treat cancer and autoimmune diseases.
XX
XX Disclosure; Fig 19; 81pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
CC can be used in the gene therapy of cancer and autoimmune diseases. The
CC present sequence is a protein described in the exemplification of the
CC invention
XX
XX Sequence 416 AA;
Query Match 52.6%; Score 219; DB 5; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.3e-208;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 HFMEVKGDLTAKWVLALLELARODRGALDCCVVILSHGCCQASHLQFPQAVYGTGCP 257
Db 198 HFMEVKGDLTAKWVLALLELARQDRGALDCCVVILSHGCCQASHLQFPQAVYGTGCP 257
QY 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEOKHGFVASTSPDESPGSPNPEPDAT 317
Db 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEOKHGFVASTSPDESPGSPNPEPDAT 317
QY 318 PFQGLRTFPQLDAISLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHS 377
Db 318 PFQGLRTFPQLDAISLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHS 377
QY 378 EDLQSLLLRVANAVSVKGIYKQMGPCFNFRLKLFKFTS 416
Db 378 EDLQSLLLRVANAVSVKGIYKQMGPCFNFRLKLFKFTS 416

RESULT 5
ADA10646
ID ADA10646 standard; protein; 416 AA.

XX ADA10646;
XX AC
XX 06-NOV-2003 (first entry)
XX Human caspase-9 protein.
XX
XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
KW ischaemic injury; cancer; autoimmune disease.
XX
XX Homo sapiens.
XX OS
XX US2002160975-A1.
XX
XX 31-OCT-2002.
XX
XX 06-FEB-2002; 2002US-00068569.
XX
XX 08-FEB-2001; 2001US-0267966P.
XX 24-AUG-2001; 2001US-00939293.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2003-219992/21.
XX N-PSDB; ADA10661.
XX
XX New nucleic acid molecules encoding a peptide or polypeptide that binds
PT to a portion of an inhibitor of apoptosis protein, useful for inducing

PT apoptosis and identifying inhibitors or enhancers of apoptosis for
PT treating AIDS, or cancer.
XX
XX Claim 36; Page 25-26; 52pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
CC polynucleotide that encodes a polypeptide or peptide, or its variants
CC that specifically binds to at least a portion of an inhibitor of
CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
CC comprising at least an N terminus sequence of caspase-9 N-terminal
CC linker sequence, a first portion of a procaspase-9 that specifically
CC binds at least a portion of an IAP and a second portion of a procaspase-9
CC containing a mutated active site, where the peptide or polypeptide
CC specifically binds at least a portion of an IAP and lacks cysteine
CC protease activity, and at least a portion of caspase-3, where the peptide
CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
CC procaspase-9, which fails to undergo normal processing and possesses wild
CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
CC expression vector comprising any of the nucleic acids, a host cell
CC containing the expression vector, an antibody that specifically binds to
CC the peptide or polypeptide, an antibody that specifically binds to an
CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the full length caspase-9 protein.
XX
XX Sequence 416 AA;

Query Match 52.6%; Score 219; DB 6; Length 416;
Best Local Similarity 99.7%; Pred. No. 2.3e-208;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 97 KLSKPTLENTTPVVLREIRKPEVLRPETPRPDVIGSGGFDVGALSLRGNADLAYILS 156
Db 97 KLSKPTLENTTPVVLREIRKPEVLRPETPRPDVIGSGGFDVGALSLRGNADLAYILS 156
QY 157 MEOGCHLIINNVNFCRESGLRTGSDICEKLRRFSSLHFMVEVKGDLTAKWVLAL 216
Db 157 MEOGCHLIINNVNFCRESGLRTGSDICEKLRRFSSLHFMVEVKGDLTAKWVLAL 216
QY 217 LELARQDHGALDCCVVVILSHGCCQASHLQFPQAVYGTGCPVSVKEIWNIFNGTSCPSLG 276
Db 217 LELARQDHGALDCCVVVILSHGCCQASHLQFPQAVYGTGCPVSVKEIWNIFNGTSCPSLG 276
QY 277 GKPKLFFIQACGGEOKHGFVASTSPDESPGSPNPEPDATPFQGLRTFDQLDAISLSP 336
Db 277 GKPKLFFIQACGGEOKHGFVASTSPDESPGSPNPEPDATPFQGLRTFDQLDAISLSP 336
QY 337 TPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGI 396
Db 337 TPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGI 396
QY 397 YKQMPGCFNRLKLFKFTS 416
Db 397 YKQMPGCFNRLKLFKFTS 416

RESULT 6
AAW39208
ID AAW39208 standard; peptide; 203 AA.
XX
XX AAW39208;
XX 18-MAY-1998 (first entry)
DT

```
XX DE Human ICE LAP-6 amino acid sequence variant.
XX
XX ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;
XX viral infection; tumour; inflammation; osteoporosis; AIDS; human;
KW Alzheimer's disease; variant.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 203
FT /note= "encoded by TAA"
XX
XX EP080904-A2.
XX
XX 26-NOV-1997.
XX
XX 19-MAY-1997; 97EP-00303397.
XX
XX 20-MAY-1996; 96US-0017949P.
XX 23-MAY-1996; 96US-0020344P.
XX 05-JUN-1996; 96US-0018961P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI ) UNIV MICHIGAN.
XX
XX Dixit VM, He W, Ruben SM, Kikly KK;
XX
XX WPI; 1998-001790/01.
XX N-PSDB; AAV09402.
XX
XX DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -
XX useful to develop products to treat, e.g. viral infection, tumour,
XX Alzheimer's disease, inflammation, osteoporosis and AIDS.
XX
XX Disclosure; Fig 5; 44pp; English.
XX
XX This is an amino acid sequence variant of human interleukin-1 beta
XX converting enzyme apoptosis protease-6 (ICE LAP-6) polypeptide. The ICE
XX LAP-6 polypeptide and agonists to the polypeptide can be used to induce
XX apoptosis, e.g. as an antiviral or antitumour agent, control embryonic
XX development and tissue homeostasis and the roles of such factors in
XX dysfunction and disease. Antagonists which inhibit the activity of the
XX ICE LAP-6 polypeptide can be used to treat, Alzheimer's or Parkinson's
XX disease, rheumatoid arthritis, septic shock, sepsis, stroke, chronic,
XX acute or central nervous system inflammation, osteoporosis, ischaemia
XX reperfusion injury, cell death associated with cardiovascular disease,
XX polycystic kidney disease, apoptosis of endothelial cells in
XX cardiovascular disease, degenerative liver disease, multiple sclerosis,
XX cerebellar degeneration, ischaemic injury, myocardial infarction,
XX acquired immunodeficiency syndrome (AIDS), myelodysplastic syndrome,
XX aplastic anaemia, male pattern baldness and head injury damage. They can
XX also be used for detection and diagnosis
XX
XX Sequence 203 AA;
XX
XX Query Match 48.6%; Score 202; DB 2; Length 203;
XX Best Local Similarity 100.0%; Pred. No. 9.1e-192;
XX Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 212 MVLALLELARQDHGALDCCVWVILSHGCOASHLPFGAVYGTGCPVSEKIVNIFNGTS 271
XX 1 MVLALLELARQDHGALDCCVWVILSHGCOASHLPFGAVYGTGCPVSEKIVNIFNGTS 60
XX
XX 272 CFSLGKPKLFTIQAGGQKDHGEVASTSPEDSPGNSNPEDATPFOEGLRTDQDA 331
XX 61 CFSLGKPKLFTIQAGGQKDHGEVASTSPEDSPGNSNPEDATPFOEGLRTDQDA 120
XX
XX 332 ISSLETPSDIFVSYSTFFPGFVSWRDPKSGSVYVETLDDIFEQWAHSEDIQSLLLRVANAV 391
XX 121 ISSLETPSDIFVSYSTFFPGFVSWRDPKSGSVYVETLDDIFEQWAHSEDIQSLLLRVANAV 180
XX
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```
QY 392 SVKGIYKOMPQCFNFKLKKFF 413
Db 181 SVKGIYKOMPQCFNFKLKKFF 202
RESULT 7
AAG67375
ID AAG67375 standard; protein; 416 AA.
XX
XX AAG67375;
XX
XX 13-NOV-2001 (first entry)
XX
XX Amino acid sequence of human Mch6 polypeptide.
XX
XX Mch6; ced-3 homologue; ICE; interleukin-1-beta converting enzyme;
XX aspartate-specific cysteine protease; ASCP; apoptotic cell death;
XX Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX retinitis pigmentosa; cerebellar degeneration; myelodysplastic syndrome;
XX aplastic anemia; ischemic injury; myocardial infarction; stroke; cancer;
XX reperfusion injury; autoimmune disease; systemic lupus erythematosus;
XX immune-mediated glomerulonephritis; viral infection; cell death.
XX
XX Homo sapiens.
XX
XX US6274318-B1.
XX
XX 14-AUG-2001.
XX
XX 13-MAY-1999; 99US-00311760.
XX
XX 29-MAY-1997; 97US-00865579.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX
XX WPI; 2001-540372/60.
XX N-PSDB; AAH77927.
XX
XX Identifying mammalian homolog ced-3 homolog (Mch)6 activity modulators,
XX useful for treating lymphomas, carcinomas and hormone dependent tumors,
XX Alzheimer's disease, Parkinson's disease, comprises using Mch6
XX polypeptide.
XX
XX Example 1; Fig 1a-c; 36pp; English.
XX
XX The present sequence represents a human Mch6 polypeptide. Mch6 is a ced-3
XX homologue, and is a member of the ICE (interleukin-1-beta converting
XX enzyme) family of aspartate-specific cysteine proteases (ASCPs). The
XX specification describes a method for identifying mammalian Mch6 activity
XX modulators (inhibitors or enhancers). The compounds identified by the
XX method are useful as pharmaceuticals for treating or preventing diseases
XX characterized by increased apoptotic cell death such as Alzheimer's
XX disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
XX pigmentosa, or cerebellar degeneration, myelodysplastic syndromes such as
XX aplastic anemia, ischemic injury including myocardial infarction, stroke
XX and reperfusion injury. The compounds are also useful for treating
XX diseases characterized by loss of apoptotic cell death such as cancers,
XX e.g. lymphomas, carcinomas and hormone dependent tumours such as breast,
XX prostate and ovarian cancer. Increased cell survival or apoptosis
XX inhibition also results in autoimmune diseases such as systemic lupus
XX erythematosus and immune-mediated glomerulonephritis as well as viral
XX infections such as herpes virus, pox virus and adenovirus and the novel
XX identified compounds are useful for treating these conditions. The Mch6
XX inhibitors are used to treat or to reduce severity of diseases
XX characterized by increased programmed cell death
XX
XX Sequence 416 AA;
```

```
Query Match 46.9%; Score 195; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.5e-184;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 222 QDHGALDCCVVVILSHGCGASHLQFPGAVVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKL 281
 Db 222 QDHGALDCCVVVILSHGCGASHLQFPGAVVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEOKDHGFVASTSPEDSPGNSPEPDATPFQEGRLRTFDQLDAISSLPTPSDI 341
 Db 282 FFIQACGGEOKDHGFVASTSPEDSPGNSPEPDATPFQEGRLRTFDQLDAISSLPTPSDI 341
 QY 342 FVSYSYTFPGFVSVWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSYTFPGFVSVWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNFLRKLFFKTS 416
 Db 402 GCFNFLRKLFFKTS 416

RESULT 8
 AAU08315
 ID AAU08315 standard; protein; 416 AA.
 XX AAU08315;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 XX Human aspartate-specific cysteine protease, MCH6.
 XX
 KW Human; aspartate-specific cysteine protease; MCH6; neurotropic;
 KW neuroprotective; anti-Parkinsonian; antianaemic; vasotropic; cardiant;
 KW cerebroprotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
 KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 KW cerebellar degeneration; myelodysplastic syndrome; aplastic anaemia;
 KW ischaemic injury; myocardial infarction; stroke; reperfusion injury;
 KW amyotrophic lateral sclerosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Active-site 285..289
 FT Cleavage-site 312..316
 FT /label= Granzyme beta_cleavage site
 FT /note= "Cleavage occurs after Asp at position 315"
 FT Cleavage-site 327..331
 FT /label= Granzyme beta_cleavage site
 FT /note= "Cleavage occurs after Asp at position 330"
 XX
 PN US2001016345-A1.
 XX
 XX 23-AUG-2001.
 XX
 XX 22-DEC-2000; 2000US-00746731.
 PF
 XX 29-MAY-1997; 97US-00865579.
 PR
 XX 25-FEB-1999; 99US-00257218.
 XX
 XX (ALNE/) ALNEMRI E S.
 PA (PERN/) FERNANDES-ALNEMRI T.
 PA (LITW/) LITWACK G.
 XX
 PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX
 XX WPI; 2001-535542/59.
 DR N-PSDB; AAS12629.
 XX
 PT New Mch6 polypeptides and genes encoding the polypeptides useful for
 PT diagnosing, treating or reducing the severity of cell death-mediated
 PT diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
 PT Parkinson's disease.
 XX
 XX Claim 8; Fig 1; 15pp; English.
 PS
 XX The invention relates to an isolated gene encoding MCH6 (mammalian ced-3

CC homologue 6) an aspartate-specific cysteine protease and the MCH6
 CC polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
 CC to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
 CC death-mediated diseases (i.e. apoptotic) such as neurodegenerative
 CC diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
 CC myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
 CC myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
 CC nucleic acids and polypeptides can also be used to diagnose or generate
 CC reagents to diagnose diseases mediated or characterised by programmed
 CC cell death. A purified recombinant MCH6 protein can be used to measure
 CC hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
 CC a continuous fluorometric assay. The present sequence represents human
 CC MCH6

XX Sequence 416 AA;

Query Match 46.9%; Score 195; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVVILSHGCGASHLQFPGAVVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKL 281
 Db 222 QDHGALDCCVVVILSHGCGASHLQFPGAVVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEOKDHGFVASTSPEDSPGNSPEPDATPFQEGRLRTFDQLDAISSLPTPSDI 341
 Db 282 FFIQACGGEOKDHGFVASTSPEDSPGNSPEPDATPFQEGRLRTFDQLDAISSLPTPSDI 341
 QY 342 FVSYSYTFPGFVSVWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSYTFPGFVSVWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNFLRKLFFKTS 416
 Db 402 GCFNFLRKLFFKTS 416

RESULT 9

AAE08938
 ID AAE08938 standard; protein; 416 AA.
 XX
 AC AAE08938;
 XX
 XX 15-NOV-2001 (first entry)
 DT
 XX Mammalian ced-3 homologue 6 (Mch6).
 DE
 XX
 KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
 KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
 KW viral infection; cell death-mediated disease; neuroprotective.

Unidentified.

XX
 XX Key Location/Qualifiers
 FH
 FT Active-site 285..290
 FT /note= "Active site pentapeptide"
 FT Cleavage-site 315..316
 FT Cleavage-site 330..331
 XX
 XX US6271361-B1.
 PN
 XX
 XX 07-AUG-2001.
 PD
 XX 25-FEB-1999; 99US-00257218.
 PF
 XX 29-MAY-1997; 97US-00865579.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;

PI Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX WPI; 2001-528686/58.
 DR N-PSDB; AAD15656.
 XX
 PT New apoptotic genes and their apoptotic protease products, useful for
 PT modulating apoptosis for the therapeutic treatment of human diseases,
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
 PT disease.
 XX
 PS Claim 2; Fig 1; 36pp; English.
 XX
 CC The invention relates to an isolated gene encoding apoptic protease,
 CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
 CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
 CC are useful for modulating apoptosis for the therapeutic treatment of
 CC human diseases. Mch6 sequences are useful for upregulating apoptosis
 CC (e.g. for treating cancers, autoimmune disease or viral infections) or
 CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
 CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
 CC useful for diagnosing, treating or reducing the severity of cell death-
 CC mediated diseases, as well as other diseases mediated by either increased
 CC or decreased programmed cell death. The present amino acid sequence is
 CC Mch6
 XX
 SQ Sequence 416 AA;
 Query Match 46.9%; Score 195; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEKIVNFGTSCPSLGGKPKL 281
 Db 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEKIVNFGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 Db 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 QY 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNFLRKKLFFKTS 416
 Db 402 GCFNFLRKKLFFKTS 416
 RESULT 10
 AAB84374
 ID AAB84374 standard; protein; 416 AA.
 AC AAB84374;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Amino acid sequence of aspartate-specific cysteine protease Mch6.
 XX
 KW Human; apoptotic protease; Mch6; aspartate-specific cysteine protease;
 KW cell death; cancer; autoimmune disease; systemic lupus erythematosus;
 KW viral infection; degenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; myelodysplastic syndrome; myocardial infarction;
 KW stroke.
 XX
 OS Homo sapiens.
 XX
 PN US2001006779-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 29-MAY-1997; 97US-00865579.
 XX
 PR 29-MAY-1997; 97US-00865579.
 XX

PA (ALNE/) ALNEMRI E S.
 PA (FERN/) FERNANDES-ALNEMRI T.
 PA (LITW/) LITWACK G.
 XX
 PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX WPI; 2001-389294/41.
 DR N-PSDB; AAH25191.
 XX
 PT Isolated gene encoding a human apoptotic protease known as Mch6, useful
 PT in the diagnosis or treatment of cell death-mediated conditions, e.g.
 PT cancers and autoimmune diseases such as systemic lupus erythematosus.
 XX
 PS Claim 8; Fig 1A-C; 15pp; English.
 XX
 CC The present sequence represents a human apoptotic protease, designated
 CC Mch6. Mch6 is an aspartate-specific cysteine protease. Mch6 polypeptides
 CC and polynucleotides can be used to diagnose, treat or reduce the severity
 CC of cell death-mediated conditions, e.g. cancers, autoimmune diseases such
 CC as systemic lupus erythematosus, viral infections such as herpesvirus,
 CC degenerative disorders such as Alzheimer's disease and Parkinson's
 CC disease, myelodysplastic syndromes such as myocardial infarction and
 CC stroke. They can also be used to screen for compounds that inhibit or
 CC promote Mch6 mediated apoptosis
 XX
 SQ Sequence 416 AA;
 Query Match 46.9%; Score 195; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEKIVNFGTSCPSLGGKPKL 281
 Db 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEKIVNFGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 Db 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 QY 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNFLRKKLFFKTS 416
 Db 402 GCFNFLRKKLFFKTS 416
 RESULT 11
 ABB82738
 ID ABB82738 standard; protein; 416 AA.
 XX
 AC ABB82738;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE Human caspase-9 polypeptide.
 XX
 KW Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human.
 XX
 OS Homo sapiens.
 XX
 PN WO20020931-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 07-MAY-2002; 2002WO-US014487.
 XX
 PR 07-MAY-2001; 2001US-0289223P.
 PR 12-FEB-2002; 2002US-0356934P.
 XX
 PA (BURN-) BURNHAM INST.
 XX

PI Reed JC;
 XX WPI; 2003-111999/10.
 XX
 PT Determining a prognosis for survival for a cancer patient, useful for
 PT determining if the patient is at risk for relapse, comprises measuring a
 PT level of TUCAN in a sample from the patient, and comparing it to a
 PT reference level.
 XX
 XX Example; Page 125-126; 153pp; English.
 XX
 CC The invention relates to determining a prognosis for survival for a
 CC cancer patient. The method involves (a) measuring a level of a tumour up-
 CC regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
 CC cell-containing sample from the cancer patient; and (b) comparing the
 CC level of TUCAN in the sample to a reference level of TUCAN, where a low
 CC level of TUCAN in the sample correlates with increased survival of the
 CC patient. Alternatively, the method involves measuring levels of TUCAN and
 CC one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
 CC Snac in a neoplastic cell-containing sample from the cancer patient. The
 CC method is useful for determining if the patient is at risk for relapse,
 CC or for determining a proper course of treatment for a patient with
 CC cancer. The method is also useful for monitoring the effectiveness of a
 CC course of treatment for a patient with cancer, e.g. colon cancer,
 CC gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
 CC leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
 CC present sequence represents a human caspase-9 polypeptide
 XX
 SQ Sequence 416 AA;
 Query Match 46.9%; Score 195; DB 6; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 Db 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 QY 282 FFIQACGGEQKDHGFVASTSPEDSPGSNPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 Db 282 FFIQACGGEQKDHGFVASTSPEDSPGSNPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 QY 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCNFKLKKLFFKTS 416
 Db 402 GCNFKLKKLFFKTS 416
 RESULT 12
 ADE52020
 ID ADE52020 standard; protein; 416 AA.
 XX
 AC ADE52020;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human mammalian ced-3 homologue 6 (Mch6).
 XX
 KW cytosolic; virucide; neurotropic; neuroprotective; antiparkinsonian;
 KW cardiant; apoptosis modulator; aspartate-specific cysteine protease;
 KW gene therapy; aspartate-specific cysteine protease agonist;
 KW aspartate-specific cysteine protease antagonist; Mch6;
 KW mammalian ced-3 homologue 6; apoptosis; cancer; viral infection;
 KW degenerative disorder; Alzheimers disease; Parkinsons disease;
 KW myocardial infarction; human; mammalian ced-3 homologue 6; Mch6.
 XX
 OS Homo sapiens.
 XX
 XX US2002189504-A1.
 FN
 XX

PD 05-DEC-2002.
 XX
 PF 29-JAN-2002; 2002US-00059749.
 XX
 PR 29-MAY-1997; 97US-00865579.
 PR 25-FEB-1999; 99US-00257218.
 PR 22-DEC-2000; 2000US-00746731.
 XX
 PA (UYJB-) UNIV JEFFERSON THOMAS.
 XX
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
 PI WPI; 2004-040943/04.
 XX
 DR New isolated gene encoding a mammalian ced-3 homolog 6, for modulating
 PT apoptosis for the therapeutic treatment of human diseases, such as
 PT cancers and degenerative disorders.
 PT
 PS Claim 8; SEQ ID NO 2; 15pp; English.
 XX
 CC The invention describes an isolated gene (I) encoding Mch6 (mammalian ced
 CC -3 homologue 6), or a functional fragment of it. (I) And the polypeptide
 CC encoded by (I) is used to modulate apoptosis for the therapeutic
 CC treatment of human diseases. (I) Is used to prepared a recombinant
 CC aspartate-specific cysteine protease, that it encodes. The recombinant
 CC protease can be used to screen for Mch6 inhibitors. Disorders involving
 CC apoptosis that can be diagnosed or treated by (I) or the polypeptide it
 CC encodes, including cancers, viral infections, degenerative disorders,
 CC such as Alzheimers and Parkinsons disease, and myocardial infarction.
 CC This is the amino acid sequence of human mammalian ced-3 homologue 6
 CC (Mch6), a member of the aspartate-specific cysteine protease (ASCP)
 CC family of proteases.
 XX
 SQ Sequence 416 AA;
 Query Match 46.9%; Score 195; DB 8; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 Db 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 QY 282 FFIQACGGEQKDHGFVASTSPEDSPGSNPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 Db 282 FFIQACGGEQKDHGFVASTSPEDSPGSNPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 QY 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCNFKLKKLFFKTS 416
 Db 402 GCNFKLKKLFFKTS 416
 RESULT 13
 AAE00620
 ID AAE00620 standard; protein; 266 AA.
 XX
 AC AAE00620;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Human caspase-9.
 XX
 KW Human; caspase-9; interleukin-1 converting enzyme; ICE-IAP6; Mch6;
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH

CC shown in the specification but was created by the indexer using the
 CC information in the claims and the wild type caspase-9 sequence.

XX Sequence 401 AA;
 SQ Query Match 29.8%; Score 124; DB 6; Length 401;
 Best Local Similarity 100.0%; Pred. No. 4.6e-114;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156
 |||||
 Db 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156
 |||||

QY 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216
 |||||
 Db 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216
 |||||

QY 217 LELA 220
 |||||
 Db 217 LELA 220
 |||||

RESULT 15

ADA10675

ID ADA10675 standard; protein; 416 AA.

XX ADA10675;

AC ADA10675;

XX 06-NOV-2003 (first entry)

DT 06-NOV-2003 (first entry)

XX Human caspase-9 protein D315A/D330A mutant.

DE Human caspase-9 protein D315A/D330A mutant.

XX Human; caspase-9; anti-HIV; nontropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; muten.

XX Synthetic.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the caspase-9 protein mutated to ablate the autocatalytic
 CC cleavage site in the linker region. Note: the present sequence is not
 CC shown in the specification but was created by the indexer using the
 CC information in the claims and the wild type caspase-9 sequence.

XX Sequence 416 AA;

SQ Sequence 416 AA;

Query Match 29.8%; Score 124; DB 6; Length 416;

Best Local Similarity 100.0%; Pred. No. 4.7e-114;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156
 |||||

Db 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156
 |||||

QY 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216
 |||||

Db 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216
 |||||

QY 217 LELA 220
 |||||

Db 217 LELA 220
 |||||

RESULT 16

ADA10676

ID ADA10676 standard; protein; 416 AA.

XX ADA10676;

AC ADA10676;

XX 06-NOV-2003 (first entry)

DT 06-NOV-2003 (first entry)

XX Human caspase-9 protein E306A/D315A/D330A mutant.

DE Human caspase-9 protein E306A/D315A/D330A mutant.

XX Human; caspase-9; anti-HIV; nontropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; muten.

XX Synthetic.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the caspase-9 protein mutated to ablate the autocatalytic
 CC cleavage site in the linker region. Note: the present sequence is not
 CC shown in the specification but was created by the indexer using the
 CC information in the claims and the wild type caspase-9 sequence.

XX SQ Sequence 416 AA;

Query Match 29.8%; Score 124; DB 6; Length 416;
 Best Local Similarity 100.0%; Pred. No. 4.7e-114;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 KLSKPTLENTTPVLRPEIRKPEVLRPETPRPDVIGSGGFDVCALESIRGNADLAYILS 156

DB 97 KLSKPTLENTTPVLRPEIRKPEVLRPETPRPDVIGSGGFDVCALESIRGNADLAYILS 156

QY 157 MEPGCHCLINNVNFCRESGLRTTGSNIDCEKLRFRFSSLHPFVVEVKGDLTAKKMWLAL 216

DB 157 MEPGCHCLINNVNFCRESGLRTTGSNIDCEKLRFRFSSLHPFVVEVKGDLTAKKMWLAL 216

QY 217 LEIA 220

DB 217 LEIA 220

RESULT 18

ABJ04760
 ID ABJ04760 standard; protein; 93 AA.

XX AC ABJ04760;

DT 16-OCT-2002 (first entry)

DE Caspase-9 protein sequence SEQ ID No 27.

XX Intracellular signaling polypeptide; Nod2; Crohn's disease; mutation;
 KW cytosine residue insertion; nuclear factor; NF-B activation; NF-kappa B;
 KW RICK signaling; gene therapy; transgenic plant; plant.

XX Homo sapiens.

XX WO200244426-A2.

XX 06-JUN-2002.

XX 26-OCT-2001; 2001WO-US051068.

XX 30-OCT-2000; 2000US-0244266P.

XX 25-APR-2001; 2001US-0286316P.

XX 26-OCT-2001; 2001US-00286316.

XX (UNMI) UNIV MICHIGAN.

XX (UYCH-) UNIV CHICAGO.

XX Nunez G, Inohara N, Ogura Y, Cho J, Nicolae DL, Bonen D;

XX WPI; 2002-547704/58.

XX New isolated intracellular signaling polypeptide, termed Nod2, useful for
 PT producing an antibody that recognizes Nod2, and as a target for screening
 PT drugs.

XX Disclosure; Fig 2; 316pp; English.

XX The invention relates to an isolated intracellular signaling polypeptide,
 CC termed Nod2, comprising a sequence of 1007 or 1040 amino acids, given in
 CC the specification. The nucleic acid encoding the isolated protein is
 CC useful for identifying subjects at risk of developing Crohn's disease by
 CC providing a nucleic acid from the subject, where the nucleic acid
 CC comprises a Nod2 gene, and detecting the presence or absence of one or
 CC more variations in the Nod2 gene. Detecting comprises comparing the

CC sequence of the nucleic acid to the sequence of a wild-type Nod2 nucleic
 CC acid. Detection is accomplished by hybridisation analysis. The method
 CC further comprises determining if the subject is at risk of developing
 CC Crohn's disease based on the presence or absence of the variations, and
 CC determining a genotype relative risk or a population attributable risk
 CC for the subject. The variation is a polymorphism or a mutation,
 CC preferably a cytosine residue insertion, where the mutation causes a
 CC deletion of a Leu-Arg-Arg repeat of Nod2. The variation results in
 CC increased nuclear factor (NF)-B activation. The variation is selected
 CC from the sequences of the Nod2 gene. The isolated protein is useful as a
 CC target for screening drugs that can alter, for example, RICK signaling,
 CC and thus the physiological effects of NF-kappa B. The Nod2 gene is useful
 CC for producing the isolated protein by recombinant techniques, as starting
 CC nucleic acids for directed evolution, for gene therapy, or to decrease
 CC the level of Nod2 protein or mRNA in transgenic plants, plant tissues, or
 CC plant cells as compared to wild-type plants, plant tissues or plant
 CC cells. This sequence represents a Nod2 related protein of the invention
 XX

XX SQ Sequence 93 AA;

Query Match 22.4%; Score 93; DB 5; Length 93;

Best Local Similarity 100.0%; Pred. No. 7.6e-84;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRRLLRRCLRLVEELQVDLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

DB 1 MDEADRRLLRRCLRLVEELQVDLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93

DB 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93

RESULT 19

ABP71130
 ID ABP71130 standard; protein; 42 AA.

XX AC ABP71130;

DT 14-APR-2003 (first entry)

XX Mch6 CARD protein fragment.

XX BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
 KW neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 KW antirheumatic; antiarthritic; gene therapy; CARD; Mch6.

XX Unidentified.

XX WO200295001-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US016230.

XX 21-MAY-2001; 2001US-0292559P.

XX (REGC) UNIV CALIFORNIA.

XX Rothman JH, Bloss T, Witze E;

XX WPI; 2003-167228/16.

XX Inhibiting or increasing programmed cell death of a cell, for treating
 PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
 PT expression or activity of basic transcription factor (BTF)3 or its
 PT homolog in the cell.

XX Example; Fig 2B; 84pp; English.

XX The invention relates to inhibiting or increasing programmed cell death
 CC of a cell. The method involves upregulating or inhibiting, respectively,
 CC the expression or activity of basic transcription factor (BTF)3 or its

CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death. The
 CC screened agent that increases or inhibits programmed cell death, is used
 CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
 CC Sequences ABP71124-135 represent peptide fragments various CARD proteins
 XX
 XX Sequence 42 AA;

Query Match 10.1%; Score 42; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-33;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GSGSRDQARQLIIDLTRGSQLPLFISCLDGTQDMLASF 88
 |||||
 Db 1 GSGSRDQARQLIIDLTRGSQLPLFISCLDGTQDMLASF 42

RESULT 20
 ADA10663
 ID ADA10663 standard; peptide; 32 AA.

AC ADA10663;
 XX
 XX 06-NOV-2003 (first entry)
 XX
 XX Human procaspase -9 amino acids 303-324.

XX caspase-9; anti-HIV; notropic; neuroprotective; vasotropic; cytostatic;
 KW immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; human.

XX Homo sapiens.
 OS
 XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

XX 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

XX Example 1; Fig 1; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated

CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents amino acids 303-324 of human procaspase-9 containing the
 CC linker region and autocatalytic sites.

XX Sequence 32 AA;

Query Match 7.7%; Score 32; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 PEDESGSNPEPDATPFQEGLTFTDQLDAISS 334
 |||||
 Db 1 PEDESGSNPEPDATPFQEGLTFTDQLDAISS 32

RESULT 21
 ADA10667

ID ADA10667 standard; peptide; 32 AA.

AC ADA10667;

XX 06-NOV-2003 (first entry)

XX Human procaspase -9 linker peptide.

XX caspase-9; anti-HIV; notropic; neuroprotective; vasotropic; cytostatic;
 KW immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; human.

XX Homo sapiens.

XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

XX 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

XX Example 3; Page 22; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of

CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents human procaspase-9 linker region.

XX SQ Sequence 32 AA;

Query Match 7.7%; Score 32; DB 6; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.1e-23;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 PEDESGNPEPDATPQEGLTDPQLDAISS 334
 |||||
 Db 1 PEDESGNPEPDATPQEGLTDPQLDAISS 32

RESULT 22

ABP71113

ID ABP71113 standard; peptide; 19 AA.

XX AC ABP71113;

XX DT 14-APR-2003 (first entry)

XX DE Mch6 protein CARD region fragment.

XX KW BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
 XX KW neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 XX KW antirheumatic; antiarthritic; gene therapy; CARD; Mch6.

XX OS Unidentified.

XX PN WO200295001-A2.

XX XX 28-NOV-2002.

XX PF 21-MAY-2002; 2002WO-US016230.

XX PR 21-MAY-2001; 2001US-0232559P.

XX XX (RBGC) UNIV CALIFORNIA.

XX PA Rothman JH, Bloss T, Witze E;

XX PI WPI; 2003-167228/16.

XX PT Inhibiting or increasing programmed cell death of a cell, for treating
 PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
 PT expression or activity of basic transcription factor (BTF)3 or its
 PT homolog in the cell.

PS Example; Fig 2A; 84pp; English.

XX CC The invention relates to inhibiting or increasing programmed cell death
 CC of a cell. The method involves upregulating or inhibiting, respectively,
 CC the expression or activity of basic transcription factor (BTF)3 or its
 CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death. The
 CC screened agent that increases or inhibits programmed cell death, is used
 CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.

CC Sequences ABP71106-123 represent CARD regions of various CARD proteins

XX SQ Sequence 19 AA;

Query Match 4.6%; Score 19; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.6e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 WDVLLSRELFRPHMIEDIQ 44
 |||||
 Db 1 WDVLLSRELFRPHMIEDIQ 19

RESULT 23

AAAY21739

ID AAY21739 standard; peptide; 15 AA.

XX AC AAY21739;

XX DT 10-SEP-1999 (first entry)

XX DE Conserved peptide sequence of Mch6 (caspase-9).

XX KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
 XX KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 XX KW tumour cell; myocardial infarction; human.

XX OS Homo sapiens.

XX PN WO9935277-A2.

XX XX 15-JUL-1999.

XX PF 11-JAN-1999; 99WO-US000632.

XX PR 09-JAN-1998; 98US-0070987P.

XX XX (UWJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES;

XX DR WPI; 1999-419353/35.

XX PT New isolated nucleic acid molecule encoding a rev-caspase - used for
 PT screening and identifying inhibitors or enhancers for treating cancer or
 PT autoimmune disease.

XX PS Disclosure; Fig 6; 74pp; English.

XX CC The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is useful for the treatment of
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful

CC for treating neurodegenerative diseases as well as for inhibiting
CC apoptosis in the heart following myocardial infarction. Sequences
CC AAY21734 -AAY21795 represent conserved peptide sequences in various
CC caspases
XX
SQ Sequence 15 AA;

Query Match 3.6%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
DB 1 GFVSWRDPKSGSWYV 15

RESULT 24
AAE08955
ID AAE08955 standard; peptide; 15 AA.

XX
AC AAE08955;
XX
DT
DE 15-NOV-2001 (first entry)
DE Mammalian ced-3 homologue 6 (Mch6) peptide fragment #6.

XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
KW viral infection; cell death-mediated disease; neuroprotective.

XX Unidentified.

XX US62711361-B1.

XX 07-AUG-2001.

XX 25-FEB-1999; 99US-00257218.

XX 29-MAY-1997; 97US-00865579.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX WPI; 2001-528686/58.

XX New apoptotic genes and their apoptotic protease products, useful for
PT modulating apoptosis for the therapeutic treatment of human diseases,
PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
PT disease.

PS Disclosure; Col 31; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease,
CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
CC are useful for modulating apoptosis for the therapeutic treatment of
CC human diseases. Mch6 sequences are useful for upregulating apoptosis
CC (e.g. for treating cancers, autoimmune disease or viral infections) or
CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
CC useful for diagnosing, treating or reducing the severity of cell death-
CC mediated diseases, as well as other diseases mediated by either increased
CC or decreased programmed cell death. The present amino acid sequence is
CC Mch6 peptide fragment

XX Sequence 15 AA;

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
DB 1 GFVSWRDPKSGSWYV 15

RESULT 25

ABJ01243

ID ABJ01243 standard; peptide; 15 AA.

XX
AC ABJ01243;

XX 18-SEP-2002 (first entry)

XX Human caspase conserved region SEQ ID NO: 59.

XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
KW autoimmune disease; cytostatic; immunosuppressive.

XX Homo sapiens.

XX US6376226-B1.

XX 23-APR-2002.

XX 26-APR-2000; 2000US-00561756.

XX 09-JAN-1998; 98US-0070897P.

XX 08-JAN-1999; 99US-00227721.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2002-453146/48.

XX New rev-caspases engineered to contain the small subunit fused in frame N
PT -terminal to the large subunit, which is in reverse order to the wild
PT type caspases, are useful to treat cancer and autoimmune diseases.

PS Disclosure; Fig 6; 81pp; English.

XX The present invention provides the protein and coding sequences of human
CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
CC can be used in the gene therapy of cancer and autoimmune diseases. The
CC present sequence is a peptide described in the exemplification of the
CC invention.

XX Sequence 15 AA;

Query Match 3.6%; Score 15; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
DB 1 GFVSWRDPKSGSWYV 15

RESULT 26

ABP71313

ID ABP71313 standard; peptide; 15 AA.

XX
AC ABP71313;

XX 28-APR-2003 (first entry)

XX Human caspase-9-p12 protein N-terminal fragment.

XX Omi; HtrA2; serine protease; inhibitor of apoptosis protein; IAP;
KW caspase; apoptosis; cytostatic; immunosuppressive; neuroprotective;
KW vasotropic; gene therapy; reaper.

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OS Homo sapiens.
XX
XX WO2003006680-A2.
XX
XX 23-JAN-2003.
XX
XX 15-JUL-2002; 2002WO-US022658.
XX
XX 13-JUL-2001; 2001US-0305378P.
XX 14-DEC-2001; 2001US-0340163P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2003-221760/21.
XX
XX New Omi nucleic acids and peptides that bind to an inhibitor of apoptosis
XX proteins, useful for regulating or altering caspase-mediated apoptosis
XX and for treating cancer, tumor, or autoimmune diseases.
XX
XX Example 2; Fig 6; 83pp; English.
XX
XX The invention relates to polynucleotides encoding an Omi (serine
XX protease) peptide or polypeptide. The Omi peptide specifically binds to a
XX portion of an inhibitor of Apoptosis Protein (IAP). The Omi polypeptide
XX induces caspase-independent apoptosis, or fails to have serine protease
XX activity. The Omi peptides are useful for regulating or altering
XX apoptosis, specifically caspase-mediated apoptosis, and as immunogens for
XX raising antibodies. Enhancers of apoptosis are useful for treating
XX cancers, tumors or for destroying cells that mediate autoimmune
XX diseases. Compositions may also be used for the treatment of diseases
XX associated with inappropriate activation of apoptosis such as
XX neurodegenerative diseases and ischaemic injury. The antibodies can be
XX used in isolating Omi peptides, polypeptides and their variants, in
XX identifying molecules that interact with Omi peptides and polypeptides,
XX and in inhibiting or enhancing the biological activity of Omi peptides
XX and polypeptides. Sequences ABP71310-315 represent fragments of various
XX IAP-binding proteins, used to determine Omi as a IAP-binding protein
XX
XX Sequence 15 AA;
SQ
Query Match 3.6%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 ATPFQEGRLTFDQLD 330
Db |||||
1 ATPFQEGRLTFDQLD 15

RESULT 27
ADA10656
ID ADA10656 standard; peptide; 15 AA.
XX
XX ADA10656;
XX
XX 06-NOV-2003 (first entry)
XX
XX Mouse caspase-9-p12 subunit N-terminus #1.
XX
XX caspase-9; anti-HIV; neurotropic; vasoprotective; cytostatic;
XX immunosuppressive; inhibitor of apoptosis protein; IAP;
XX caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
XX Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
XX ischaemic injury; cancer; autoimmune disease; mouse; p12 subunit.
XX
XX Mus musculus.
XX
XX OS
XX US2002160975-A1.
XX
XX 31-OCT-2002.
XX

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PF 06-FEB-2002; 2002US-00068569.
XX
XX 08-FEB-2001; 2001US-0267966P.
XX 24-AUG-2001; 2001US-00939293.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2003-219992/21.
XX
XX New nucleic acid molecules encoding a peptide or polypeptide that binds
XX to a portion of an inhibitor of apoptosis protein, useful for inducing
XX apoptosis and identifying inhibitors or enhancers of apoptosis for
XX treating AIDS, or cancer.
XX
XX Claim 27; Fig 9; 52pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically
XX binds at least a portion of an IAP and a second portion of a procaspase-9
XX containing a mutated active site, where the peptide or polypeptide
XX specifically binds at least a portion of an IAP and lacks cysteine
XX protease activity, and at least a portion of caspase-3, where the peptide
XX or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
XX an IAP or an IAP Bir3 domain) or at least a portion of a mutated
XX procaspase-9, which fails to undergo normal processing and possesses wild
XX type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
XX polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
XX expression vector comprising any of the nucleic acids, a host cell
XX containing the expression vector, an antibody that specifically binds to
XX the peptide or polypeptide, an antibody that specifically binds to an
XX epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
XX in a cell or stimulating apoptosis in a neoplastic or tumour cell,
XX identifying an inhibitor or enhancer of caspase-mediated apoptosis,
XX identifying a compound that inhibits the peptide or polypeptide,
XX producing a compound for inhibiting or enhancing apoptosis in a cell, and
XX a process for the manufacture of a compound for inhibiting or enhancing
XX apoptosis in a cell. The nucleic acid molecules and peptides or
XX polypeptides are useful for inducing apoptosis and identifying inhibitors
XX or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
XX ischaemic injury, cancer, autoimmune diseases. The present sequence
XX represents the N-terminus of an IAP protein containing a Bir3 domain.
XX
XX Sequence 15 AA;
SQ
Query Match 3.6%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 ATPFQEGRLTFDQLD 330
Db |||||
1 ATPFQEGRLTFDQLD 15

RESULT 28
ADA10651
ID ADA10651 standard; peptide; 15 AA.
XX
XX ADA10651;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human caspase-9-p12 subunit N-terminus #1.
XX
XX caspase-9; anti-HIV; neurotropic; neuroprotective; vasotrophic; cytostatic;
XX immunosuppressive; inhibitor of apoptosis protein; IAP;
XX caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
XX Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
XX
XX

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KW ischaemic injury; cancer; autoimmune disease; Human; p12 subunit.

OS Homo sapiens.

XX US2002160975-A1.

PN 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

PR 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

PA Alnemri ES;

PI WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds to a portion of an inhibitor of apoptosis protein, useful for inducing apoptosis and identifying inhibitors or enhancers of apoptosis for treating AIDS, or cancer.

XX Claim 27; Fig 9; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a polynucleotide that encodes a polypeptide or peptide, or its variants that specifically binds to at least a portion of an inhibitor of apoptosis protein (IAP). Also included are a peptide or a polypeptide (comprising at least an N terminus sequence of caspase-9 N-terminal linker sequence, a first portion of a procaspase-9 that specifically binds at least a portion of an IAP and a second portion of a procaspase-9 containing a mutated active site, where the peptide or polypeptide specifically binds at least a portion of an IAP and lacks cysteine protease activity, and at least a portion of caspase-3 where the peptide or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by an IAP or an IAP Bir3 domain) or at least a portion of a mutated procaspase-9, which fails to undergo normal processing and possesses wild type caspase-9 enzymatic activity, a nucleic acid molecule comprising a polynucleotide sequence that encodes the caspase-9 N-terminal linker), an expression vector comprising any of the nucleic acids, a host cell containing the expression vector, an antibody that specifically binds to the peptide or polypeptide, an antibody that specifically binds to an epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis in a cell or stimulating apoptosis in a neoplastic or tumour cell, identifying an inhibitor or enhancer of caspase-mediated apoptosis, identifying a compound that inhibits the peptide or polypeptide, producing a compound for inhibiting or enhancing apoptosis in a cell, and a process for the manufacture of a compound for inhibiting or enhancing apoptosis in a cell. The nucleic acid molecules and peptides or polypeptides are useful for inducing apoptosis and identifying inhibitors or enhancers of apoptosis for treating AIDS, neurodegenerative diseases, ischaemic injury, cancer, autoimmune diseases. The present sequence represents the N-terminus of an IAP protein containing a Bir3 domain.

XX Sequence 15 AA;

Query Match 3.6%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFQEGRLTFQOLD 330
DB 1 ATPFQEGRLTFQOLD 15

RESULT 29

AAE08939

ID AAE08939 standard; peptide; 46 AA.

XX AAE08939;

AC AAE08939;

XX

DT 15-NOV-2001 (first entry)

XX Mammalian ced-3 homologue 6 (Mch6) peptide.

XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer; aspartate-specific cysteine protease; ASCP; apoptosis; therapy; autoimmune disease; cerebellar degeneration; Alzheimer's disease; cytostatic; Parkinson's disease; immunomodulator; antimicrobial; viral infection; cell death-mediated disease; neuroprotective.

XX Unidentified.

XX US6271361-B1.

PN 07-AUG-2001.

XX 25-FEB-1999; 99US-00257218.

XX 29-MAY-1997; 97US-00865579.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX WPI; 2001-528686/58.

XX New apoptotic genes and their apoptotic protease products, useful for modulating apoptosis for the therapeutic treatment of human diseases, e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's disease.

XX Example 1; Fig 2; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease, mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences are useful for modulating apoptosis for the therapeutic treatment of human diseases. Mch6 sequences are useful for upregulating apoptosis (e.g. for treating cancers, autoimmune disease or viral infections) or downregulating apoptosis (e.g. for treating Alzheimer's disease, Parkinson's disease or cerebellar degeneration). The Mch6 sequence is useful for diagnosing, treating or reducing the severity of cell death-mediated diseases, as well as other diseases mediated by either increased or decreased programmed cell death. The present amino acid sequence is Mch6 peptide

XX Sequence 46 AA;

Query Match 3.6%; Score 15; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
DB 32 GFVSWRDPKSGSWYV 46

RESULT 30

ADE52024

ID ADE52024 standard; protein; 46 AA.

XX ADE52024;

XX 29-JAN-2004 (first entry)

XX Aspartate-specific cysteine protease Mch6 fragment.

XX cytosolic; virucide; neurotropic; neuroprotective; antiparkinsonian; cardiant; apoptosis modulator; aspartate-specific cysteine protease; gene therapy; aspartate-specific cysteine protease agonist; aspartate-specific cysteine protease antagonist; Mch6; mammalian ced-3 homologue 6; apoptosis; cancer; viral infection; degenerative disorder; Alzheimers disease; Parkinsons disease;

KW myocardial infarction; human; ASPC.
 XX Homo sapiens.
 OS
 PN US2002183504-A1.
 XX
 XX
 PD 05-DEC-2002.
 XX
 XX 29-JAN-2002; 2002US-00059749.
 XX
 XX 29-MAY-1997; 97US-00865579.
 PR
 PR 25-FEB-1999; 99US-00257218.
 PR
 PR 22-DEC-2000; 2000US-00746731.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
 PI
 XX WPI; 2004-040943/04.
 DR
 XX New isolated gene encoding a mammalian ced-3 homolog 6, for modulating
 PT apoptosis for the therapeutic treatment of human diseases, such as
 PT cancers and degenerative disorders.
 PT
 XX
 XX Example 1; SEQ ID NO 6; 15pp; English.
 PS
 XX The invention describes an isolated gene (I) encoding Mch6 (mammalian ced
 CC -3 homologue 6), or a functional fragment of it. (I) And the polypeptide
 CC encoded by (I) is used to modulate apoptosis for the therapeutic
 CC treatment of human diseases. (I) Is used to prepared a recombinant
 CC aspartate-specific cysteine protease, that it encodes. The recombinant
 CC protease can be used to screen for Mch6 inhibitors. Disorders involving
 CC apoptosis that can be diagnosed or treated by (I) or the polypeptide it
 CC encodes, including cancers, viral infections, degenerative disorders,
 CC such as Alzheimers and Parkinsons disease, and myocardial infarction.
 CC This is the amino acid sequence of a human aspartate-specific cysteine
 CC protease (ASCP) fragment used in a comparison with other ASCP family
 CC members.
 CC
 XX Sequence 46 AA;
 SQ
 Query Match 3.6%; Score 15; DB 8; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 GFVSWRDPKSGSWTV 364
 |||||
 DB 32 GFVSWRDPKSGSWTV 46
 |||||
 RESULT 31
 AAM97045
 ID AAM97045 standard; peptide; 14 AA.
 XX
 AC AAM97045;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #320 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 PF
 XX

PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US035498.
 XX
 PR 28-DEC-1999; 99US-0173419P.
 PR
 PR 27-DEC-2000; 2000US-00173419.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach M;
 PI
 XX WPI; 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PR oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 PT
 XX
 XX Disclosure; Page 3738; 4143pp; English.
 PS
 XX The present invention relates to oligonucleotides (see AAL26793-AA134659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiopoietin, apoptosis-related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 XX
 SQ Sequence 14 AA;
 Query Match 3.4%; Score 14; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 FRPHMIEDIQRAGS 48
 |||||
 DB 1 FRPHMIEDIQRAGS 14
 |||||
 RESULT 32
 AAU08321
 ID AAU08321 standard; peptide; 15 AA.
 XX
 AC AAU08321;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human MCH6 conserved sequence #6.
 XX
 KW Human; aspartate-specific cysteine protease; MCH6; nootropic;
 KW neuroprotective; anti-Parkinsonian; antianemic; vasotropic; cardiant;
 KW cerebrotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
 KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 KW cerebellar degeneration; myelodysplastic syndrome; aplastic anaemia;
 KW ischaemic injury; myocardial infarction; stroke; reperfusion injury;
 KW amyotrophic lateral sclerosis; conserved sequence.
 XX
 OS Homo sapiens.
 XX
 PN US2001016345-A1.
 XX
 PD 23-AUG-2001.
 XX
 PF 22-DEC-2000; 2000US-00746731.
 XX


```

PR 29-MAY-1997; 97US-00865579.
PR 25-FEB-1999; 99US-00257218.
PA (ALNE//) ALNEMRI E S.
PA (FERN//) FERNANDES-ALNEMRI T.
PA (LITW//) LITWACK G.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX
XX WPI; 2001-535542/59.
XX
XX New Mch6 polypeptides and genes encoding the polypeptides useful for
XX diagnosing, treating or reducing the severity of cell death-mediated
XX diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
XX Parkinson's disease.
XX
XX Example 1; Fig 2; 15pp; English.
XX
XX The invention relates to an isolated gene encoding MCH6 (mammalian ced-3
XX homologue 6) an aspartate-specific cysteine protease and the MCH6
XX polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
XX to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
XX death-mediated diseases (i.e. apoptotic) such as neurodegenerative
XX diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
XX lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
XX myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
XX myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
XX nucleic acids and polypeptides can also be used to diagnose or generate
XX reagents to diagnose diseases mediated or characterised by programmed
XX cell death. A purified recombinant MCH6 protein can be used to measure
XX hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
XX a continuous fluorometric assay. The present sequence represents a
XX conserved sequence from human MCH6 indicating that MCH6 is a member of
XX the Ced-like subfamily of proteases
XX
XX Sequence 15 AA;
XX
XX Query Match 2.9%; Score 12; DB 4; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.0004;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 350 GFVSWRDPKSGS 361
XX |||||
XX Db 1 GFVSWRDPKSGS 12
XX
XX RESULT 33
XX AA89198
XX ID AA89198 standard; protein; 299 AA.
XX
XX AC AA89198;
XX
XX DT 17-MAR-1999 (first entry)
XX
XX DE Aspartate-specific cysteine protease, Caspase-1.
XX
XX KW Caspase-1; Spodoptera frugiperda; Sf; insect; nuclear immunophilin;
XX CED-3 subfamily; aspartate-specific cysteine protease; ASCP; apoptosis.
XX
XX OS Spodoptera frugiperda.
XX
XX Key Location/Qualifiers
XX FH Cleavage-site 28..29
XX FT Cleavage-site 184..185
XX FT Cleavage-site 195..196
XX
XX PN US5858778-A.
XX
XX PD 12-JAN-1999.
XX
XX PF 27-DEC-1996; 96US-00773608.
XX
XX PS 27-DEC-1996; 96US-00773608.
XX

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XX
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX PI Litwack G, Alnemri ES, Fernandes-Alnemri T;
XX
XX DR WPI; 1999-119894/10.
XX DR N-PSDB; AAV80061.
XX
XX PT Isolated aspartate-specific cysteine protease; Caspase-1 - obtained from
XX Spodoptera frugiperda, used to develop screening assays for compounds
XX which can inhibit or enhance apoptosis.
XX
XX PS Claim 1; Fig 1A; 22pp; English.
XX
XX CC This represents a Caspase-1 pro-enzyme, a novel Spodoptera frugiperda
XX (Sf) insect cell nuclear immunophilin which belongs to the CED-3
XX subfamily of aspartate-specific cysteine proteases (ASCPs). A host cell
XX containing an expression vector comprising the Caspase-1 nucleic acid can
XX be used for the recombinant production of the protein. The products can
XX be used for screening for compounds which can inhibit or enhance Caspase-
XX 1 activity and which can be used to inhibit or enhance, respectively,
XX apoptosis. The Caspase-1 can also be used to identify proteins which are
XX processed by it. The products can also be used for the production of
XX antibodies and for the production of transgenic animals
XX
XX SQ Sequence 299 AA;
XX
XX Query Match 2.6%; Score 11; DB 2; Length 299;
XX Best Local Similarity 100.0%; Pred. No. 0.055;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 277 GKPKLFFIQAC 287
XX |||||
XX Db 168 GKPKLFFIQAC 178
XX
XX RESULT 34
XX ABB61468
XX ID ABB61468 standard; protein; 323 AA.
XX
XX AC ABB61468;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster polypeptide SEQ ID NO 11196.
XX
XX KW Drosophila; developmental biology; cell signaling; insecticide;
XX pharmaceutical.
XX
XX OS Drosophila melanogaster.
XX
XX PN WO200171042-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX
XX PA (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-658860/75.
XX DR N-PSDB; ABL05571.
XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX PS Disclosure; SEQ ID NO 11196; 21pp + Sequence Listing; English.
XX

```

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 323 AA;

Query Match 2.6%; Score 11; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPRLFIOAC 287
|||
Db 186 GKPRLFIOAC 196
|||

RESULT 35
ABB58379
ID ABB58379 standard; protein; 339 AA.
AC ABB58379;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 1929.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX N-PSDB; ABL02482.
XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 1929; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

Query Match 2.6%; Score 11; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 0.062; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 277 GKPRLFIOAC 287
|||
Db 201 GKPRLFIOAC 211
|||

RESULT 36
ABP71122
ID ABP71122 standard; peptide; 10 AA.
XX
XX AC ABP71122;

XX
XX 14-APR-2003 (first entry)
XX
XX Mch6 protein CARD region fragment.
DE

XX BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
XX neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
XX antirheumatic; antiarthritic; gene therapy; CARD; Mch6.
XX
XX Unidentified.

XX WO200295001-A2.
XX
XX 28-NOV-2002.
XX

XX 21-MAY-2002; 2002WO-US016230.
XX
XX 21-MAY-2001; 2001US-0292559P.
XX
XX (REGC) UNIV CALIFORNIA.

XX Rothman JH, Bloss T, Witze E;
XX
XX WPI; 2003-167228/16.
XX

XX Inhibiting or increasing programmed cell death of a cell, for treating
PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
PT expression or activity of basic transcription factor (BTF)3 or its
PT homolog in the cell.
XX
XX Example; Fig 2A; 84pp; English.

PS The invention relates to inhibiting or increasing programmed cell death
CC of a cell. The method involves upregulating or inhibiting, respectively,
CC the expression or activity of basic transcription factor (BTF)3 or its
CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
CC for inhibiting or increasing programmed cell death. They are used for
CC screening for an agent that increases or inhibits programmed cell death
CC or pre-screening for an agent that modulates programmed cell death. The
CC screened agent that increases or inhibits programmed cell death, is used
CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
XX Sequences ABP71106-123 represent CARD regions of various CARD proteins
XX
XX Sequence 10 AA;

Query Match 2.4%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 RDOARQLIID 61
|||
Db 1 RDOARQLIID 10
|||

RESULT 37
AAM68529
ID AAM68529 standard; protein; 163 AA.
XX


```

QY      278 KPQLFFIQAC 287
Db      84 KPQLFFIQAC 93

RESULT 39
AAB98655
ID      AAB98655 standard; protein; 244 AA.
XX
XX      AC
XX      AAB98655;
XX
XX      16-AUG-2001 (first entry)
XX
XX      Caspase-7.
XX
XX      Caspase-1; Protein co-ordinate data; caspase-7; S4 binding region;
XX      caspase-3.
XX
XX      Unidentified.
XX
XX      WO200137194-A2.
XX
XX      25-MAY-2001.
XX
XX      16-NOV-2000; 2000WO-US031602.
XX
XX      16-NOV-1999; 99US-0165797P.
XX
XX      (VERT-) VERTEX PHARM INC.
XX
XX      Wei Y;
XX
XX      WPI; 2001-329229/34.
XX
XX      Molecule or molecular complex used for drug discovery, comprises a
XX      binding pocket of caspase-7 or a homolog having an S4 binding region more
XX      hydrophilic than that of caspase-3.
XX
XX      Example 4; Fig 3; 161pp; English.
XX
XX      The present invention relates to a molecule or molecular complex (1)
XX      comprising a binding pocket defined by the structure coordinates of
XX      caspase-7 amino acids 234, 235, 237, 276, 278, 281, and 284 or a homolog
XX      of (1) with a binding pocket having a root mean square deviation from the
XX      amino acid backbone atoms of not more than 1.5 Angstrom, where (1) has an
XX      S4 binding region that is more hydrophilic than that of caspase-3. The
XX      present sequence is caspase-7, which was used in a sequence homology
XX      alignment
XX
XX      SQ      Sequence 244 AA;
XX
XX      Query Match      2.4%; Score 10; DB 4; Length 244;
XX      Best Local Similarity 100.0%; Pred. No. 0.46;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPQLFFIQAC 287
Db      118 KPQLFFIQAC 127

RESULT 40
AAB15262
ID      AAB15262 standard; protein; 303 AA.
XX
XX      AC
XX      AAB15262;
XX
XX      05-AUG-1997 (first entry)
XX
XX      Apoptotic protease Mch3-alpha.
XX
XX      Mch3-alpha; cysteine protease; apoptosis; AIDS; ischaemia;
XX      neurodegenerative disease; therapy; diagnosis.
XX
XX      KW
XX      Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptosis;

```

```

OS      Homo sapiens.
XX
XX      Key
XX      Domain
XX
XX      Location/Qualifiers
XX      1..198
XX      /label= P20
XX      /note= "p20 subunit"
XX      24..28
XX      /label= P20
XX      54..58
XX      /label= P17
XX      99..103
XX      /label= P12
XX      184..188
XX      /note= "QACRG active site"
XX      199..303
XX      /label= P12
XX      /note= "p12 subunit"
XX
XX      WO9718313-A1.
XX
XX      22-MAY-1997.
XX
XX      12-NOV-1996; 96WO-US018118.
XX
XX      13-NOV-1995; 95US-00556627.
XX
XX      (IDUN-) IDUN PHARM INC.
XX      (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX      Alnemri ES, Fernandes-Alnemri T, Litwack G, Armstrong R;
XX      Tomaselli K;
XX
XX      WPI; 1997-289289/26.
XX      N-PSDB; AAT66992.
XX
XX      New gene encoding Mch3, a cysteine protease that regulates apoptosis -
XX      for treating human diseases associated with apoptosis, and screening for
XX      antagonists and agonists of Mch3.
XX
XX      Claim 8; Fig 1; 52pp; English.
XX
XX      Human Mch3-alpha (AAW15262) is an apoptotic protein and novel member of
XX      the interleukin-1-beta converting enzyme (ICE) family of cysteine
XX      proteases. Its amino acid sequence was deduced from a cDNA clone
XX      (AAT66992) obt'd. from a Jurkat library. Mch3-beta (AAW15263) has also
XX      been identified that lacks the active site of Mch3-alpha. Mch3-alpha
XX      polypeptides can be produced in engineered host cells and used to treat
XX      human diseases associated with cell death, such as AIDS, ischaemic
XX      injury, neurodegenerative diseases, etc. They can also be used to
XX      regulate apoptosis and to screen for Mch3 agonists and antagonists
XX
XX      SQ      Sequence 303 AA;
XX
XX      Query Match      2.4%; Score 10; DB 2; Length 303;
XX      Best Local Similarity 100.0%; Pred. No. 0.55;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPQLFFIQAC 287
Db      177 KPQLFFIQAC 186

RESULT 41
AAB15247
ID      AAB15247 standard; protein; 303 AA.
XX
XX      AC
XX      AAB15247;
XX
XX      21-JUL-1997 (first entry)
XX
XX      Cysteine protease CMH-1.
XX
XX      Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptosis;

```

KW programmed cell death; cancer; neurodegenerative disease;
 KW autoimmune disease; gene therapy; diagnosis.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Pro-peptide
 FT Protein 24..303
 FT /label= Mat.protein
 FT /note= "active CMH-1 polypeptide (Claim 3)"
 FT 29..303
 FT Protein /label= Mat.protein
 FT /note= "active CMH-1 polypeptide (Claim 3)"
 FT 155
 FT Active-site /note= "His144 is a catalytic residue"
 FT 186
 FT Active-site /note= "Cys186 is a catalytic residue"

XX WO9716552-A1.

PN 09-MAY-1997.

XX 01-NOV-1996; 96WO-US017431.

XX 03-NOV-1995; 95US-0007211P.

PR 06-NOV-1995; 95US-0007251P.

PR 16-NOV-1995; 95US-00558733.

XX (VERT-) VERTEX PHARM INC.

XX Su M, Lippke JA;

XX WPI; 1997-272121/24.

DR N-PSDB; AA166970.

XX DNA encoding active, activatable or inactive cysteine protease CMH-1 -
 PT useful in gene therapy for promoting and inhibiting apoptosis and for
 PT diagnosing cells with potential for apoptosis.

PS Claim 3; Page 32-33; 48pp; English.

XX A proenzyme (AAW15247) is activated to CMH-1, or CPP32/Mch2 homologue-1,
 CC a human cysteine protease that is involved in apoptosis. Its amino acid
 CC sequence was deduced from a full-length isolated cDNA clone (AA166970).
 CC Active, activatable (i.e. proenzyme) or inactivated forms of CMH-1 can be
 CC expressed in prokaryotic or eukaryotic host cells. The polypeptides are
 CC useful for screening potential apoptosis inhibitors and for raising
 CC antibodies used to assay CMH-1, to regulate cholesterol levels, inhibit
 CC CMH-1 activity and therefore apoptosis, and to purify CMH-1 polypeptides

XX Sequence 303 AA;

Query Match 2.4%; Score 10; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 KPFLFFIQAC 287

Db 177 KPFLFFIQAC 186

RESULT 42

AAAY21721

ID AAY21721 standard; protein; 303 AA.

XX AAY21721;

AC AAY21721;

XX 10-SEP-1999 (first entry)

XX Amino acid sequence of caspase-7 (Mch3).

DE Rev-caspase; cysteine protease; zymogen; cancer; gene therapy;

XX

KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 KW tumour cell; myocardial infarction; human.

XX Homo sapiens.

XX WO9935277-A2.

PN 15-JUL-1999.

XX 11-JAN-1999; 99WO-US000632.

XX 09-JAN-1998; 98US-0070987P.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 1999-419353/35.

XX N-PSDB; AAX81223.

XX New isolated nucleic acid molecule encoding a rev-caspase - used for
 screening and identifying inhibitors or enhancers for treating cancer or
 autoimmune disease.

XX Disclosure; Fig 17A-B; 74pp; English.

XX The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is useful for the treatment of
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful
 CC for treating neurodegenerative diseases as well as for inhibiting
 CC apoptosis in the heart following myocardial infarction. Sequences
 CC AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
 CC gene products (AAY21715-Y21724)

XX Sequence 303 AA;

Query Match 2.4%; Score 10; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 KPFLFFIQAC 287

Db 177 KPFLFFIQAC 186

RESULT 43

AAE00604

ID AAE00604 standard; protein; 303 AA.

XX AAE00604;

XX 02-JUL-2001 (first entry)

XX Human caspase-7.

XX Human; caspase-7; interleukin-1 converting enzyme; ICE-LAP3; CHM-1; Mch3;
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 23..24

XX /label= Proteolytic_cleavage_site

XX Cleavage-site 198..199

```
FT Cleavage-site /label= Proteolytic_cleavage_site
FT 206..207
FT /label= Proteolytic_cleavage_site
XX
XX WO200129232-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-US028941.
XX
XX 20-OCT-1999; 99US-0160559P.
XX
XX 14-AUG-2000; 2000US-0225564P.
XX
XX (SCIO-) SCIOS INC.
XX
XX Cordell B, Li Y;
XX
XX WPI; 2001-290920/30.
XX
XX N-PSDB; AAD03914.
XX
XX Novel fusion polypeptide comprising first and second caspase subunit
XX separated by cleavage site not associated in nature with caspase subunit,
XX useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage.
XX
XX Claim 4; Fig 14; 116pp; English.
XX
XX The present amino acid sequence is human Caspase-7 also known as
XX interleukin-1 converting enzyme (ICE) LAP3, CHM-1 and Mhc3. Caspases are
XX a family of cysteine proteases, that participate in the initiation and
XX execution of apoptosis. Caspases exist as pro-enzymes, activated by
XX cleavage into a large and small subunit, occurring after specific
XX aspartic acid residues within the pro-enzyme sequence. The present
XX invention relates to a method for functional cloning of genes encoding
XX proteins or enzymes involved in proteolytic cleavage. The invention is
XX based on the use of caspase expression cassettes comprising the coding
XX sequence of a proteolytic cleavage site flanked by sequences encoding two
XX caspase subunits. A fusion polypeptide comprising a first and a second
XX caspase subunit, separated by a cleavage site not associated in nature,
XX is useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage. An expression cassette containing fusion polypeptide is used to
XX identify a mutant cell line deficient in an enzyme of interest and is
XX also useful for diagnosis and suppression of proliferation or metastases
XX of a tumour cell characterised by overexpression of a polypeptide (e.g.
XX Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
XX encoding fusion polypeptide is used in gene therapy
XX
XX Sequence 303 AA;
XX
XX Query Match 2.4%; Score 10; DB 4; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
XX QY 278 KPKLFFFIQAC 287
XX |||||
XX Db 177 KPKLFFFIQAC 186
XX
XX RESULT 44
XX ABJ01222
XX ID ABJ01222 standard; protein; 303 AA.
XX
XX AC ABJ01222;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human caspase-7 SEQ ID NO: 24.
XX
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
XX autoimmune disease; cytostatic; immunosuppressive.
XX
XX Homo sapiens.
XX
XX PT
```

```
PN US6376226-B1.
XX
XX 23-APR-2002.
XX
XX 26-APR-2000; 2000US-00561756.
XX
XX 09-JAN-1998; 98US-0070897P.
XX
XX 08-JAN-1999; 99US-00227721.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-453146/48.
XX
XX N-PSDB; ABO3970.
XX
XX New rev-caspases engineered to contain the small subunit fused in frame N
XX -terminal to the large subunit, which is in reverse order to the wild
XX type caspases, are useful to treat cancer and autoimmune diseases.
XX
XX Disclosure; Fig 17; 81pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
XX can be used in the gene therapy of cancer and autoimmune diseases. The
XX present sequence is a protein described in the exemplification of the
XX invention
XX
XX Sequence 303 AA;
XX
XX Query Match 2.4%; Score 10; DB 5; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
XX QY 278 KPKLFFFIQAC 287
XX |||||
XX Db 177 KPKLFFFIQAC 186
XX
XX RESULT 45
XX ABB78588
XX ID ABB78588 standard; protein; 303 AA.
XX
XX AC ABB78588;
XX
XX 15-JUL-2002 (first entry)
XX
XX Mouse caspase 7 protein sequence SEQ ID NO:97.
XX
XX Caspase 7; antisense modulation; antiinflammatory; cytostatic;
XX antisense therapy; caspase 7 inhibitor; inflammatory condition;
XX hyperproliferative disorder; cancer; bone metabolism; infection;
XX cholesterol disorder; inflammation; tumour.
XX
XX Mus musculus.
XX
XX WO200222640-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028232.
XX
XX 11-SEP-2000; 2000US-00659860.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX WPI; 2002-404806/43.
XX
XX N-PSDB; ABN80919.
XX
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
XX for modulating gene expression and treating diseases associated with
XX
```

PT expression of caspase 7 in humans.
 PS Example 16; Page 121-123; 138pp; English.
 XX
 CC The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding caspase 7, which
 CC specifically hybridises with and inhibits the expression of caspase 7.
 CC (I) has antiinflammatory and cytostatic activities, and can be used in
 CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
 CC useful for inhibiting the expression of caspase 7 in human cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with caspase 7 including inflammatory condition,
 CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
 CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as
 CC research reagent and kits. (I) is useful prophylactically to prevent or
 CC delay infection, inflammation or tumour formation. The present sequence
 CC represents a mouse caspase 7 protein, which is used in an example from
 CC the present invention
 XX
 SQ Sequence 303 AA;

Query Match 2.4%; Score 10; DB 5; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
 |||||
 Db 177 KPXLFFFIQAC 186

RESULT 46
 ABB09299
 ID ABB09299 standard; protein; 303 AA.

AC ABB09299;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human caspase 7 protein sequence SEQ ID NO:17.

XX
 KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
 KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
 KW hyperproliferative disorder; cancer; bone metabolism; infection;
 KW cholesterol disorder; inflammation; tumour.

XX Homo sapiens.

XX WO200222640-A1.

XX 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US028232.

PR 11-SEP-2000; 2000US-00659860.

PA (ISIS-) ISIS PHARM INC.

PI Zhang H, Watt AT;

XX WPI; 2002-404806/43.

DR N-PSDB; ABN80839.

XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
 PT for modulating gene expression and treating diseases associated with
 PT expression of caspase 7 in humans.

PS Example 15; Page 101-103; 138pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding caspase 7, which
 CC specifically hybridises with and inhibits the expression of caspase 7.
 CC (I) has antiinflammatory and cytostatic activities, and can be used in
 CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is

CC useful for inhibiting the expression of caspase 7 in human cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with caspase 7 including inflammatory condition,
 CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
 CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as
 CC research reagent and kits. (I) is useful prophylactically to prevent or
 CC delay infection, inflammation or tumour formation. The present sequence
 CC represents a human caspase 7 protein, which is used in an example from
 CC the present invention
 XX
 SQ Sequence 303 AA;

Query Match 2.4%; Score 10; DB 5; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
 |||||
 Db 177 KPXLFFFIQAC 186

RESULT 47
 ABB09297
 ID ABB09297 standard; protein; 303 AA.

AC ABB09297;

XX 15-JUL-2002 (first entry)

DE Human caspase 7 protein sequence SEQ ID NO:3.

XX Caspase 7; antisense modulation; antiinflammatory; cytostatic;
 KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
 KW hyperproliferative disorder; cancer; bone metabolism; infection;
 KW cholesterol disorder; inflammation; tumour.

OS Homo sapiens.

XX WO200222640-A1.

XX 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US028232.

PR 11-SEP-2000; 2000US-00659860.

PA (ISIS-) ISIS PHARM INC.

PI Zhang H, Watt AT;

XX WPI; 2002-404806/43.

DR N-PSDB; ABN80825.

XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
 PT for modulating gene expression and treating diseases associated with
 PT expression of caspase 7 in humans.

PS Example 13; Page 94-96; 138pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding caspase 7, which
 CC specifically hybridises with and inhibits the expression of caspase 7.
 CC (I) has antiinflammatory and cytostatic activities, and can be used in
 CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
 CC useful for inhibiting the expression of caspase 7 in human cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with caspase 7 including inflammatory condition,
 CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
 CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as
 CC research reagent and kits. (I) is useful prophylactically to prevent or
 CC delay infection, inflammation or tumour formation. The present sequence
 CC represents a human caspase 7 protein, which is used in an example from
 CC the present invention

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XX SQ Sequence 303 AA;
Query Match 2.4%; Score 10; DB 5; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
Db 177 KPKLFFFIQAC 186

RESULT 48
AAO19868
ID AAO19868 standard; protein; 303 AA.
XX AC AAO19868;
XX DT 11-AUG-2003 (first entry)
XX DE Bacteriophage caspase 7 protein.
XX KW Bacteriophage; lytic; pathogenic bacterium; phage; annihilation moiety;
XX KW infection; tuberculosis; AIDS; HIV infection; malaria; mutagenic;
XX KW tuberculostatic; anti-HIV; virucide; protozoacide; antibacterial.
XX OS Bacteriophage.
XX PN WO2003000274-A2.
XX PD 03-JAN-2003.
XX PF 21-JUN-2002; 2002WO-GB002879.
XX PR 22-JUN-2001; 2001GB-00015385.
XX PA (REGM-) REGMA BIO TECHNOLOGIES LTD.
XX PA (POLY/) POLYANSKAYA N.
XX PI Pasechnik V, West D;
XX WPI; 2003-210119/20.
XX DR N-PSDB; ABZ69367.
XX PT Bacteriophage preparation for stimulating death of infected cell, has
XX PT bacteriophage that enters cell and lyses pathogenic bacteria that infect
XX PT cells, linked to annihilation moiety that stimulates death of infected
XX PT cells.
XX PS Disclosure; Page 21; 45pp; English.
XX CC The present invention relates to a bacteriophage preparation, comprising
XX CC a bacteriophage modified to enter eukaryotic cells, which is lytic to
XX CC pathogenic bacterial strain infecting the cell, and is capable of
XX CC expressing an annihilation moiety. Said moiety will then cause the death
XX CC or inactivation of an infected cell. In particular, the preparation can
XX CC be used to kill cells infected with tuberculosis, HIV, AIDS and malaria.
XX CC The present sequence is a protein produced by a DNA fragment used to
XX CC produce the modified bacteriophage of the invention
XX SQ Sequence 303 AA;
Query Match 2.4%; Score 10; DB 6; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
Db 177 KPKLFFFIQAC 186

RESULT 49
ABB69920
ID ABB69920 standard; protein; 308 AA.
XX AC ABB69920;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 36552.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL14023.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 36552; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 308 AA;
Query Match 2.4%; Score 10; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
Db 162 KPKLFFFIQAC 171

RESULT 50
ABB09300
ID ABB09300 standard; protein; 336 AA.
XX AC ABB09300;
XX DT 15-JUL-2002 (first entry)
XX DE Human caspase 7 protein sequence SEQ ID NO:18.
XX KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
XX KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
XX KW hyperproliferative disorder; cancer; bone metabolism; infection;
XX KW cholesterol disorder; inflammation; tumour.
XX OS Homo sapiens.

```



```
XX WO200222640-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028232.
XX
XX 11-SEP-2000; 2000US-00659860.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX WPI; 2002-404806/43.
XX
XX N-PSDB; ABN80840.
XX
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
XX for modulating gene expression and treating diseases associated with
XX expression of caspase 7 in humans.
XX
XX Example 15; Page 103-105; 138pp; English.
XX
XX The present invention describes a compound (I) 8-50 nucleobases in length
XX targeted to a nucleic acid molecule encoding caspase 7, which
XX specifically hybridizes with and inhibits the expression of caspase 7.
XX (I) has antiinflammatory and cytostatic activities, and can be used in
XX antisense therapy and as an inhibitor of caspase 7 expression. (I) is
XX useful for inhibiting the expression of caspase 7 in human cells or
XX tissues, and for treating a human having a disease or condition
XX associated with caspase 7 including inflammatory condition,
XX hyperproliferative disorder (cancer), or bone metabolism or cholesterol
XX disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as
XX research reagent and kits. (I) is useful prophylactically to prevent or
XX delay infection, inflammation or tumour formation. The present sequence
XX represents a human caspase 7 protein, which is used in an example from
XX the present invention
XX
XX Sequence 336 AA;
SQ
Query Match 2.4%; Score 10; DB 5; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 278 KPKLFFIQAC 287
Db 210 KPKLFFIQAC 219
|||||
|||||
Search completed: August 3, 2004, 09:09:29
Job time : 57 secs
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:03:42 ; Search time 13 Seconds
(without alignments)
1666.245 Million cell updates/sec

Title: US-09-961-201A-1
Perfect score: 416
Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKQMGCCFNLRKLFKTS 416

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219	52.6	416	1	ICE9_HUMAN
2	11	2.6	299	1	ICE1_SPOFR
3	11	2.6	333	1	ICE1_DROME
4	11	2.6	339	1	ICE1_DROME
5	10	2.4	303	1	ICE7_HUMAN
6	10	2.4	303	1	ICE7_MESAU
7	10	2.4	303	1	ICE7_MOUSE
8	10	2.4	521	1	ICEA_HUMAN
9	9	2.2	484	1	CFLA_MOUSE
10	9	2.2	1196	1	BR11_ARATH
11	8	1.9	232	1	YK10_ARCFU
12	8	1.9	579	1	Y876_MYCLE
13	8	1.9	1207	1	BR11_LYCES
14	8	1.9	1207	1	BR11_LYCPPE
15	8	1.9	1393	1	RPOC_CHLPN
16	7	1.7	132	1	GCSH_MYCLE
17	7	1.7	180	1	PTH_CHLPN
18	7	1.7	196	1	HNK2_XENLA
19	7	1.7	210	1	GIDB_RHILLO
20	7	1.7	264	1	RS3_RALSO
21	7	1.7	274	1	NHS_STRAS
22	7	1.7	306	1	SDSB_PSES9
23	7	1.7	338	1	G3P_THEVO
24	7	1.7	345	1	TRPD_AERPE
25	7	1.7	349	1	TRUD_SALTI
26	7	1.7	349	1	TRUD_SALTI
27	7	1.7	401	1	RA17_YEAST
28	7	1.7	404	1	YBR3_YEAST
29	7	1.7	420	1	BACA_RHIME
30	7	1.7	426	1	LIP7_CANAL
31	7	1.7	437	1	RECA_TROWT
32	7	1.7	442	1	IFR2_HUMAN
33	7	1.7	480	1	ICE8_MOUSE

34	7	1.7	487	1	PHOQ_SALTY
35	7	1.7	503	1	VRK2_MOUSE
36	7	1.7	504	1	PSD5_HUMAN
37	7	1.7	505	1	SPKD_SYNY3
38	7	1.7	508	1	VRK2_HUMAN
39	7	1.7	548	1	SYK_HALNI
40	7	1.7	551	1	E2K2_HUMAN
41	7	1.7	575	1	GGT_PSESP
42	7	1.7	628	1	LU_HUMAN
43	7	1.7	664	1	UL47_HSVLP
44	7	1.7	749	1	TR2M_AGRRH
45	7	1.7	755	1	TR2M_AGR74
46	7	1.7	755	1	TR2N_AGRVI
47	7	1.7	778	1	YQ34_MYCTU
48	7	1.7	805	1	HIFA_XENLA
49	7	1.7	1011	1	CAPP_SYNEL
50	7	1.7	1062	1	UL70_HCMVA
51	7	1.7	1507	1	Y056_HUMAN
52	7	1.7	1997	1	OTOF_HUMAN
53	7	1.7	3119	1	CA1C_MOUSE
54	7	1.7	3259	1	G0B1_HUMAN
55	6	1.4	45	1	ATI2_HSVB4
56	6	1.4	67	1	G0N1_MCMU
57	6	1.4	71	1	YQKK_BACSU
58	6	1.4	84	1	NTXP_TITSE
59	6	1.4	84	1	SCX7_TITBE
60	6	1.4	84	1	SCX7_TITSE
61	6	1.4	84	1	SCX7_TITST
62	6	1.4	87	1	Y32A_MYCGE
63	6	1.4	89	1	SLTB_BPH30
64	6	1.4	90	1	G0N1_MOUSE
65	6	1.4	91	1	G0N1_PIG
66	6	1.4	92	1	G0N1_CAVPO
67	6	1.4	92	1	G0N1_HUMAN
68	6	1.4	92	1	G0N1_TUPGB
69	6	1.4	95	1	IHF8_RHOCA
70	6	1.4	97	1	PY_DICLA
71	6	1.4	98	1	ACYO_HUMAN
72	6	1.4	98	1	ACYO_MOUSE
73	6	1.4	100	1	ACYO_PIG
74	6	1.4	104	1	RS17_THETH
75	6	1.4	110	1	ETS2_LYTVA

ALIGNMENTS

RESULT 1	
ICE9_HUMAN	STANDARD; PRT; 416 AA.
ID	P55211; O95348; Q92852; Q9B062; Q9UEQ3; Q9ULV8;
AC	DT 01-OCT-1996 (Rel. 34, Created)
DT	DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT	DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE	Caspase-9 precursor (BC 3.4.22.-) (CASP-9) (ICE-like apoptotic
DE	protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic
DE	activating factor 3) (APAF-3).
GN	CASP9 OR MCH6.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.
RX	MEDLINE=96279246; PubMed=8663294;
RA	Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,
RA	He W.-W., Dixit V.M.;
RT	ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated
RT	by the cytotoxic T cell protease granzyme B.;
RL	J. Biol. Chem. 271:16720-16724 (1996).
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.
RC	TISSUE=T-cell;

RX MEDLINE=97059171; PubMed=8900201.
 RA Srinivasula S.M., Fernandez-Alnemri T., Zangrilli J., Robertson N.,
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
 RA Alnemri E.S.;
 RA "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
 RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
 RT mediator CPP32."; 
 RL J. Biol. Chem. 271:27099-27106(1996).
 RL [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99315341; PubMed=10384055;
 RA Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P.,
 RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;
 RA "Genomic organization of the human caspase-9 gene on chromosome
 RT 1p36.1-p36.3";
 RL Mamm. Genome 10:757-760(1999).
 RL [4]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99168502; PubMed=10070954;
 RA Srinivasula S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,
 RA Fernandez-Alnemri T., Alnemri E.S.;
 RA "Identification of an endogenous dominant-negative short isoform of
 RT caspase-9 that can regulate apoptosis.";
 RL Cancer Res. 59:999-1002(1999).
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP TISSUE=Stomach cancer;
 RC Izawa M., Mori T., Ito H., Sairenji T.;
 RA "Molecular cloning and sequencing of a cDNA predicting an alternative
 RT form of pro-caspase-9 from human gastric cancer cell lines.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP Mho Y., Momoi T., Fujita E.;
 RA "A novel splicing product of human caspase-9 lacking protease
 RT activity";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RN SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT VAL-28.
 RP MEDLINE=99107856; PubMed=9890966;
 RA Seol D.W., Billiar T.R.;
 RA "A caspase-9 variant missing the catalytic site is an endogenous
 RT inhibitor of apoptosis.";
 RL J. Biol. Chem. 274:2072-2076(1999).
 RL [8]
 RN SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28; LEU-99; ILE-102;
 RP VAL-106; ASP-114; HIS-173 AND ARG-221.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RL [9]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RA Thomas D.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL [10]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong I.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Baha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,
 RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.

```

DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02009; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02007; CASPASE_P10; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW Polymorphism; 3D-structure.
FT CHAIN ? 315
FT PROPEP 316 330
FT CHAIN 331 416
FT DOMAIN 1 92
FT ACT_SITE 237 237
FT ACT_SITE 287 287
FT VARSPLIC 140 289
FT VARIANT 28 28
FT VARIANT 99 99
FT VARIANT 102 102
FT VARIANT 106 106
FT VARIANT 114 114
Query Match 52.6%; Score 219; DB 1; Length 416;
Best Local Similarity 99.7%; Pred. No. 2.4e-215;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 97 KLSKPTLENTPVVLREIKRPEVLRPETRPVDIGSGFGDVGALSLRGNADLAYILS 156
Db 97 KLSKPTLENTPVVLREIKRPEVLRPETRPVDIGSGFGDVGALSLRGNADLAYILS 156
QY 157 MFCGHCILINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHFMVEVKGDLTAKGVVAL 216
Db 157 MFCGHCILINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHFMVEVKGDLTAKGVVAL 216
QY 217 LELAQDHGALDCVVVILSHGQASHLPFGAVGTGDCPVSVKIVNFNGTSCPSLG 276
Db 217 LELAQDHGALDCVVVILSHGQASHLPFGAVGTGDCPVSVKIVNFNGTSCPSLG 276
QY 277 GKPLFFIOACGGEQKHGFVASTSPDESPGSNPEPDATPFQEGRLTFDQLDAISSLP 336
Db 277 GKPLFFIOACGGEQKHGFVASTSPDESPGSNPEPDATPFQEGRLTFDQLDAISSLP 336
QY 337 TSDIFVSYSTPFGVSWRDPKSGSWYVETLDDIFQWASHEDLQSLLRVANAVSKGI 396
Db 337 TSDIFVSYSTPFGVSWRDPKSGSWYVETLDDIFQWASHEDLQSLLRVANAVSKGI 396
QY 397 YKQMPGCFNFKRKKLFFKTS 416
Db 397 YKQMPGCFNFKRKKLFFKTS 416

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RESULT 2

```

ID ICEL_SPOFR STANDARD; PRT; 299 AA.
AC P89116;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-).
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrae; Spodoptera.
OX NCBI_TaxID=7108;

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```

RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97153084; PubMed=8999805;
RA Ahmad M., Srinivasula S.M., Wang L., Litwack G., Fernandes-Alnemri T.,
RA Alnemri E.S.;
RT "Spodoptera frugiperda caspase-1, a novel insect death protease that
RT cleaves the nuclear immunophilin FKBP46, is the target of the
RT baculovirus antiapoptotic protein p35.";
RL J. Biol. Chem. 272:1421-1424(1997).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution (By similarity). Inhibited by
CC the baculovirus anti-apoptotic protein p35. Cleaves p35 and
CC nuclear immunophilin FKBP46.
CC -!- SUBUNIT: Heterodimer of a 19/18 kDa (p19/18) and a 12 kDa (p12)
CC subunit.
CC -!- PTM: AN AUTOCATALYTIC MECHANISM GENERATES THE TWO ACTIVE SUBUNITS.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U81510; AAC47442.1; -.
CC HSPP; P42574; ICP3.
CC MEROPS; C14.015; -.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC InterPro; IPR002398; Peptidase C14.
CC Pfam; PF00656; Peptidase C14; 1.
CC PRINTS; PR00376; IL1BCENZYM.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS02007; CASPASE_P10; 1.
CC PROSITE; PS02008; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1 28
FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.
FT PROPEP 185 195 POTENTIAL.
FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.
FT ACT_SITE 136 136 BY SIMILARITY.
FT ACT_SITE 178 178 BY SIMILARITY.
SQ SEQUENCE 299 AA; 33527 MW; 99F4FED09B04EEDC CRC64;
Query Match 2.6%; Score 11; DB 1; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 277 GKPLFFIOAC 287
Db 169 GKPLFFIOAC 178

```

RESULT 3

```

ID ICEL_DROME STANDARD; PRT; 323 AA.
AC O02002; Q9W1N0;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-).
GN DCP-1 OR CG5370.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.

```

RC TISSUE=Embryo;
RX MEDLINE=97153052; PubMed=8999799;
RA Song Z., McCall K., Steller H.;
RT "DCP-1, a Drosophila cell death protease essential for development.";
RL Science 275:536-540(1997).
RN [2]
RP ERRATUM.
RA Song Z., McCall K., Steller H.;
RL Science 277:167-167(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Buser D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Minkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Embryo;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacle J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.E.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution (By similarity).
CC Proteolytically cleaves poly(ADP-ribose) polymerase (PARP). Loss
CC of zygotic DCP-1 function causes larval lethality and melanotic
CC tumors.
CC -!- SUBUNIT: Heterodimer of a 22 kDa (p22) and a 13 kDa (p13) subunit.
CC -!- DEVELOPMENTAL STAGE: Present uniformly throughout embryos of
CC stages 4 and 10. In stage 16 embryos, the expression becomes
CC restricted to the central nervous system, the developing gonads,
CC and a portion of the gut. In stage 17 embryos, expression is
CC mainly localized in cells along the midline of the central nervous
CC system.

CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF001464; AAB58237.1; -;
DR EMBL; AE003461; AAF47027.1; -;
DR EMBL; BT010065; AAQ22534.1; -;
DR HSP; P42574; 1PAU.
DR MEROPS; C14.016; -;
DR FlyBase; FBgn0010501; Dcp-1.
DR GO; GO:004199; F:caspase activity; IDA.
DR GO; GO:0004207; F:effector caspase activity; NAS.
DR GO; GO:0030036; F:actin cytoskeleton organization and biogenesis; IMP.
DR GO; GO:0008632; P:apoptotic program; IDA.
DR GO; GO:0006922; P:cleavage of lamin; IMP.
DR GO; GO:0009795; P:embryonic morphogenesis; IMP.
DR GO; GO:0007300; P:nurse cell/oocyte transport (sensu Insecta); IMP.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BENZZYME.
DR SMART; SM01115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 33 PROBABLE.
FT CHAIN 34 202 CASPASE-1 SUBUNIT P22.
FT PROPEP 203 215 CASPASE-1 SUBUNIT P13.
FT CHAIN 216 323 BY SIMILARITY.
FT ACT_SITE 154 154 BY SIMILARITY.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35926 MW; B5FF0FF75EB0E2BD CRC64;
Query Match 2.6%; Score 11; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 277 GKPKLFFFIQAC 287
DB 186 GKPKLFFFIQAC 196
RESULT 4
ICE DROME
ID ICE_DROME STANDARD; PRT; 339 AA.
AC 001382; Q9VAH1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase precursor (EC 3.4.22.-) (dRICE).
GN ICE OR CG7788.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97327558; PubMed=9184225;
RA Fraser A.G., Evan G.I.;
RT "Identification of a Drosophila melanogaster ICE/CED-3-related
RT protease, dRICE";
RL EMBO J. 16:2805-2813(1997).

RN SEQUENCE FROM N.A.
 RC STRAIN=Berkeley.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.O., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Hwang J., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Head;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A *Drosophila* full-length cDNA resource."
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Acts downstream of rpr.
 CC Cleaves baculovirus p35 and lamin Dmo in vitro.
 CC -!- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
 CC -!- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
 CC occurs.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Y12261; CAA72937.1; -;
 DR EMBL; AE003771; AAF56939.1; -;
 DR EMBL; AY058451; AAL13680.1; -;
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.015; -;
 DR FlyBase; FBgn0019972; Ice.

DR GO; GO:0004207; F:effector caspase activity; NAS.
 DR GO; GO:0006915; P:apoptosis; NAS.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILICENZYME.
 DR SMART; SM01115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS02027; CASPASE_F10; 1.
 DR PROSITE; PS02028; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 28
 FT CHAIN 29 217
 FT PROPEP 218 230
 FT CHAIN 231 339
 FT ACT_SITE 169 169
 FT ACT_SITE 211 211
 FT CONFLICT 151 151
 FT CONFLICT 265 265
 FT CONFLICT S -> T (IN REF. 1).
 SQ SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;
 Query Match 2.6%; Score 11; DB 1; Length 339;
 Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 GKPKLRFIQAC 287
 DB 201 GKPKLRFIQAC 211
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 RESULT 5
 ICE7 HUMAN STANDARD; PRT; 303 AA.
 ID PS5210; Q13364; Q96BA0;
 AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-7 precursor (BC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).
 GN CASP7 OR MCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=96139498; PubMed=8576161;
 RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
 RA Dixit V.M.;
 RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
 RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
 RT factor-induced apoptosis."
 RL J. Biol. Chem. 271:1621-1625(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Spleen;
 RX MEDLINE=96147144; PubMed=8567622;
 RA Lipke J.A., Gu Y., Sarnecki C., Caron P.R., Su M.S.-S.;
 RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
 RT cysteine protease similar to CPP32."
 RL J. Biol. Chem. 271:1825-1828(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=F-cell;
 RX MEDLINE=96105019; PubMed=8521391;
 RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
 RA Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvesson G.,
 RA Earnshaw W.C., Litwack G., Alnemri E.S.;
 RT "Mch3, a novel human apoptotic cysteine protease highly related to
 RT CPP32."
 RL Cancer Res. 55:6045-6052(1995).

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
 DE (SCA-2).
 GN CASP7 OR MCH3.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=SYRIAN; TISSUE=Liver;
 RA MEDLINE=96224303; PubMed=8643593;
 RX Pai J.-T., Brown M.S., Goldstein J.L.;
 RT "Purification and cDNA cloning of a second apoptosis-related cysteine
 RT protease that cleaves and activates sterol regulatory element binding
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Cleaves and activates sterol
 CC regulatory element binding proteins (SREBPs). Proteolytically
 CC cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
 CC bond. Overexpression promotes programmed cell death (By
 CC similarity).
 CC -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC
 CC -----
 CC EMBL: U47332; AAC52595.1; -;
 CC HSSP: P42574; 1PAU.
 CC
 CC MEROFS; C14.004; -;
 CC InterPro: IPR002138; ICE_p10.
 CC InterPro: IPR001309; ICE_p20.
 CC InterPro: IPR002398; Peptidase C14.
 CC Pfam: PF00656; Peptidase C14; 1.
 CC PRINTS: PR00376; ILBENZYM.E.
 CC SMART: SM00115; CASC; 1.
 CC PROSITE: PS01122; CASPASE_CYS; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 CC PROSITE: PS0207; CASPASE_P10; 1.
 CC PROSITE: PS0208; CASPASE_P20; 1.
 CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
 CC PROPEP 1 23
 CC FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
 CC FT PROPEP 199 206 BY SIMILARITY.
 CC FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
 CC FT ACT_SITE 144 144 BY SIMILARITY.
 CC FT ACT_SITE 186 186 BY SIMILARITY.
 CC SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;
 Query Match 2.4%; Score 10; DB 1; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 278 KPFLFFIQAC 287
 |||||||

Db 177 KPFLFFIQAC 186
 RESULT 7
 ICE7 MOUSE
 ID ICE7 MOUSE STANDARD; PRT; 303 AA.
 AC P97864; O08669;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
 DE protease Mch-3).
 DE CASP7 OR MCH3 OR LICE2.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA MEDLINE=97224489; PubMed=9070923;
 RX Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93(1997).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=97236307; PubMed=9125129;
 CC Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
 CC Momoi T.;
 CC "Wortmannin enhances CPP32-like activity during neuronal
 CC differentiation of P19 embryonal carcinoma cells induced by retinoic
 CC acid.";
 CC Biochem. Biophys. Res. Commun. 232:192-197(1997).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C3H/An;
 CC MEDLINE=97190206; PubMed=9038361;
 CC van de Craen M., Vandenaabeele P., Declercq W., van den Brande I.,
 CC van Loo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
 CC Fiers W.;
 CC "Characterization of seven murine caspase family members.";
 CC FEBS Lett. 403:61-69(1997).
 CC [4]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=22388257; PubMed=12477932;
 CC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
 CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 CC Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 CC "Generation and initial analysis of more than 15,000 full-length
 CC human and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Cleaves and activates sterol
 CC regulatory element binding proteins (SREBPs). Overexpression
 CC promotes programmed cell death (By similarity).
 CC -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

TISSUE=T-cell;
MEDLINE=96353838; PubMed=8755496;
Fernandes-Alnemri T., Armstrong R. C., Krebs J., Srinivasula S. M.,
Wang L., Bullrich F., Fritz L. C., Trapani J. A., Tomaselli K. J.,
Litwack G., Alnemri E. S.;
"In vitro activation of CPP32 and Mch3 by Mch4, a novel human
apoptotic cysteine protease containing two FADD-like domains";
Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
[2]
SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE=97197836; PubMed=9045686;
Vincenz C., Dixit V. M.;
"Fas-associated death domain protein interleukin-1beta-converting
enzyme 2 (FICD2), an ICD/Ced-3 homologue, is proximally involved in
CD95- and p55-mediated death signaling";
J. Biol. Chem. 272:6578-6583(1997).
[3]
SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT ILE-410.
TISSUE=Spleen, and Thymus;
MEDLINE=99214592; PubMed=10187817;
Ng P. W., Porter A. G., Janicke R. U.;
"Molecular cloning and characterization of two novel pro-apoptotic
isoforms of caspase-10";
J. Biol. Chem. 274:10301-10308(1999).
[4]
SEQUENCE FROM N.A. (ISOFORMS A AND B).
MEDLINE=21100893; PubMed=11161814;
Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
Martindale D., Koop B. F., Scherer S. W., Nicholson D. W., Rouleau G. A.,
Ikeda J. E., Hayden M. R.;
"Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
critical region at chromosome 2q33-q34: candidate genes for ALS2";
Genomics 71:200-213(2001).
[5]
PARTIAL SEQUENCE, AND PROCESSING.
MEDLINE=97121412; PubMed=8962078;
Srinivasula S. M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
Alnemri E. S.;
"Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
protease Mch5 is a CrmA-inhibitable protease that activates multiple
Ced-3/Ccr-1-like cysteine proteases";
Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
[6]
VARIANT ALPS2 PHE-285, AND VARIANT ILE-410.
MEDLINE=99339325; PubMed=10412980;
Wang J., Zheng L., Lobito A. A., Chan F. K., Dale J., Sneller M., Yao X.,
Puck J. M., Straus S. E., Lenardo M. J.;
"Inherited human caspase 10 mutations underlie defective lymphocyte
and dendritic cell apoptosis in autoimmune lymphoproliferative
syndrome type II";
Cell 98:47-58(1999).
-!- FUNCTION: Involved in the activation cascade of caspases
responsible for apoptosis execution. Recruited to both Fas- and
TNFR1 receptors in a FADD dependent manner. May participate in
the granzyme B apoptotic pathways. Cleaves and activates caspase-
3, -4, -6, -7, -8, and -9. Hydrolyzes the small-molecule
substrates, Tyr-Val-Ala-Asp-|-AMC and Asp-Glu-Val-Asp-|-AMC.
-!- SUBSTRATES: Isoform C is proteolytically inactive.
-!- SUBUNIT: Heterodimer of a 23/17 kDa (p23/17) depending on the
splicing events and a 12 kDa (p12) subunit.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=A; Synonyms=10-A;
IsoId=Q32851-1; Sequence=Displayed;
Name=B; Synonyms=10-B;
IsoId=Q32851-2; Sequence=VSP_000819, VSP_000820;
Name=C; Synonyms=10-C;
IsoId=Q32851-3; Sequence=VSP_000821, VSP_000822;
-!- TISSUE SPECIFICITY: Detectable in most tissues. Lowest expression
is seen in brain, kidney, prostate, testis and colon.
-!- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE
THE TWO ACTIVE SUBUNIT.

length and shorter isoforms have been shown either to induce apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic (caspase) activity (By similarity).

- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-inducing signaling complex (DISC) formed by TNFRSF6, FADD and caspase-8. A proteolytic fragment (p43) stays associated with the DISC (By similarity).

- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1; Synonyms=FLIP-L, CASH alpha;

Isoid=035732-1; Sequence=Displayed;

Name=2; Synonyms=FLIP-S, CASH beta;

Isoid=035732-2; Sequence=VSP_000842, VSP_000843;

TISSUE SPECIFICITY: Highly expressed in heart.

DEVELOPMENTAL STAGE: At embryonic days E9.5 and E10.5 highest expression in developing heart.

- INDUCTION: Isoform 1 but not isoform 2 is activated by BCR cross-linking in primary B-cells.

- DOMAIN: The caspase domain lacks the active sites residues involved in catalysis.

- PTM: Proteolytically processed; probably by caspase-8. Processing likely occurs at the DISC, generates subunit p43 and p12 (By similarity).

- SIMILARITY: Belongs to peptidase family C14.

- SIMILARITY: Contains 2 death effector (DED) domains.

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EMBL: Y14041; CAA74368.1; -

DR EMBL: Y14042; CAA74369.1; -

DR EMBL: U97076; AAC53281.1; -

DR HSP: Q15806; IQDU.

DR MEROPS: C14.974; -

MGD: MGI:1336166; Cflar.

InterPro: IPR001875; DED.

InterPro: IPR001309; ICE p20.

InterPro: IPR002398; Peptidase_C14.

Pfam: PF01335; DED; 2.

Pfam: PF00656; Peptidase_C14; 1.

SMART: SM00115; CASC; 1.

SMART: SM00031; DED; 2.

PROSITE: PS50208; CASPASE_P20; 1.

PROSITE: PS50168; DED; 2.

Apoptosis; Repeat; Alternative splicing.

CHAIN	1	380
CHAIN	381	484
DOMAIN	6	78
DOMAIN	97	175
DOMAIN	266	363
DOMAIN	421	425
VARSPLIC	208	218

FT FT CHAIN 1 380 CASP8 AND FADD-LIKE APOPTOSIS REGULATOR

FT FT SUBUNIT P43 (BY SIMILARITY).

FT FT CASP8 AND FADD-LIKE APOPTOSIS REGULATOR

FT FT SUBUNIT P12 (BY SIMILARITY).

FT FT DED 1.

FT FT DED 2.

FT FT CASPASE.

FT FT POLY-SER.

FT FT LQNGRSKEPRF -> VSLPVPVGVPA (in isoform 2).

FT FT /FTId=VSP_000842.

FT FT Missing (in isoform 2).

FT FT /FTId=VSP_000843.

FT FT MISSING (IN REF. 2).

FT FT SEQUENCE 484 AA; 55245 MW; 0BF7A92CB09F5F1F CRC64;

Query Match 2.2%; Score 9; DB 1; Length 484;

Best Local Similarity 100.0%; Pred. No. 0.67;

Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY	277	GKPKLFFIQ	285
Db	355	GKPKLFFIQ	363

RESULT 10

BR11-ARATH STANDARD; PRT; 1196 AA.

ID BR11-ARATH

AC O22476;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE BRASSINOSTEROID INSENSITIVE 1 precursor (EC 2.7.1.37) (AtBR11)

DE (Brassinosteroid LRR receptor kinase).

DE BR11 OR AT4G39400 OR F23K16.30.

GN Arabidopsis thaliana (Mouse-ear cress).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

NCBI_TaxID=3702;

FX

FN

SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND MUTANTS BR11-101; BR11-104; BR11-113 AND BR11-115.

RC STRAIN=cv. Columbia;

RC MEDLINE=97442355; PubMed=9298904;

EX Li J., Chory J.,

RT "A putative leucine-rich repeat receptor kinase involved in brassinosteroid signal transduction."

RL Cell 90:929-938 (1997).

[2]

SEQUENCE FROM N.A., FUNCTION, AND MUTANTS BR11-5/DWF2-W41; BR11-6/BR11-119/DWF2-399; BR11-7/DWF2-WM3-2; BR11-8/DWF2-WM6-2 AND BR11-9/DWF2-WB19.

RC STRAIN=cv. Massilewskija-2, and cv. En-2;

RC MEDLINE=20027415; PubMed=10557222;

EX Noguchi T., Fujioka S., Choe S., Takatsuto S., Yoshida S., Yuan H., Feldmann K.A., Tax F.E.,

RA "Brassinosteroid-insensitive dwarf mutants of Arabidopsis accumulate brassinosteroids."

RT Plant Physiol. 121:743-752 (1999).

[3]

SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MUTANTS BR11-1; BR11-108; BR11-117 AND BR11-102.

RC STRAIN=cv. Columbia;

RC MEDLINE=20398322; PubMed=10938344;

EX Friedrichsen D.M., Joazeiro C.A.P., Li J., Hunter T., Chory J.,

RA "BRASSINOSTEROID-INSENSITIVE-1 is a ubiquitously expressed leucine-rich repeat receptor serine/threonine kinase."

RT Plant Physiol. 123:1247-1256 (2000).

[4]

SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RC MEDLINE=20083488; PubMed=10617198;

EX Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delsen Y.M., Puigdomenech P., Watson M., Schmidheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Kidley P., Langham S.-A., McCullagh B., Bilham L., Robben J., Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F., Braeken M., Wajtjens I., Voet M., Bastiaens I., Aert R., Defoor E., Weitzenegger I., Bothe G., Ramsperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., De Keyser A., Buysschaert C., Gielen J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S., Clark L., Doggett J., Hall S., Kay M., Lennard N., Mclay K., Mayes R., Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H., Dose S., de Haan M., Maarse A.C., Schaefer K., Mueller-Auer S., Gabel C., Fuchs M., Partmann B., Grandeth K., Dauner D., Herzl A., Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,

RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedfor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mix P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Marra M.A., Martienssen R., McCombie W.R.,
 RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RA thaliana".
 RT Nature 402:769-777(1999).
 RL [5]
 RN PHOSPHORYLATION.
 RP MEDLINE=20484044; PubMed=11027724;
 RX Oh M.-H., Ray W.K., Huber S.C., Asara J.M., Gage D.A., Clouse S.D.;
 RA "Recombinant BRASSINOSTEROID INSENSITIVE 1 receptor-like kinase
 RT autophosphorylates on serine and threonine residues and
 RT phosphorylates a conserved peptide motif in vitro";
 RL Plant Physiol. 124:751-766(2000).
 RN [6]
 RP STEROID BINDING.
 RP MEDLINE=20336852; PubMed=10875920;
 RX He Z., Wang Z.-Y., Li J., Zhu Q., Lamb C., Ronald P., Chory J.;
 RA "Perception of brassinosteroids by the extracellular domain of the
 RT receptor kinase BRI1";
 RL Science 288:2360-2363(2000).
 RN [7]
 RP SUBCELLULAR LOCATION, STEROID BINDING, AND AUTOPHOSPHORYLATION.
 RP MEDLINE=21168182; PubMed=11268216;
 RX Wang Z.-Y., Seto H., Fujioaka S., Yoshida S., Chory J.;
 RA "BRI1 is a critical component of a plasma-membrane receptor for plant
 RT steroids";
 RL Nature 410:380-383(2001).
 RN [8]
 RP SUBCELLULAR LOCATION, PHOSPHORYLATION, AND INTERACTION WITH BAK1.
 RP MEDLINE=22145926; PubMed=12150928;
 RX Nam K.H., Li J.;
 RA "BRI1/BAK1, a receptor kinase pair mediating brassinosteroid
 RT signaling";
 RL Cell 110:203-212(2002).
 RN [9]
 RP PHOSPHORYLATION, AND INTERACTION WITH BAK1.
 RP MEDLINE=22145927; PubMed=12150929;
 RX Li J., Wen J., Lease K.A., Duke J.T., Tax F.E., Walker J.C.;
 RA "BAK1, an Arabidopsis LRR receptor-like protein kinase, interacts with
 RT BRI1 and modulates brassinosteroid signaling";
 RL Cell 110:213-222(2002).
 CC -!- FUNCTION: Receptor with a serine/threonine-protein kinase
 CC activity. Regulates, in response to brassinosteroid binding, a
 CC signaling cascade involved in plant development, including
 CC elongation of light- and stress-regulated genes, promotion of cell
 CC elongation, normal leaf and chloroplast senescence, and flowering.
 CC Binds brassinolide, and less effectively castasterone, but not
 CC 2,3,22,23-O-tetramethylbrassinolide or ecdysone. May be involved
 CC in a feedback regulation of brassinosteroid biosynthesis.
 CC Phosphorylates BRI1-associated receptor kinase 1 (BAK1).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- ENZYME REGULATION: Activated by Ser and Thr phosphorylation.
 CC -!- SUBUNIT: Heterodimer with BAK1.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- TISSUE SPECIFICITY: Expressed ubiquitously.

CC -!- DEVELOPMENTAL STAGE: Expressed constitutively in either dark- or
 CC light-grown seedlings.
 CC -!- DOMAIN: Contains one leucine-zipper motif and two pairs of
 CC conservatively spaced Cys (Cys pair 1 and 2) involved in forming
 CC heterodimers.
 CC -!- PTM: Phosphorylated on at least 12 sites, with a preference for
 CC Ser residues.
 CC -!- MISCELLANEOUS: A 70 amino acid island between the 20th and the
 CC 21th LRR is essential for the binding of brassinosteroids.
 CC -!- MISCELLANEOUS: Binding of brassinosteroid induces intramolecular
 CC autophosphorylation of BRI1. Interaction with BAK1 activates both
 CC receptor kinases and the full activation of either receptor kinase
 CC requires transphosphorylation by their partners. Optimum in vitro
 CC phosphorylation of the substrate requires Arg or Lys residues at
 CC P-3, P-4, and P-5 (relative to the phosphorylated amino acid at
 CC P-0).
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC -!- SIMILARITY: Contains 25 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 CC EMBL: AF017056; AAC49810.1; -
 CC EMBL: AL078820; CAB44675.1; -
 CC EMBL: AL161595; CAB80603.1; -
 CC PIR: T09356; T09356.
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR007090; LRR_plant.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR008271; Ser_thr_pkin_AS.
 CC InterPro: IPR001245; Tyr_pkinase.
 CC Pfam: PF00560; LRR; 17.
 CC Pfam: PF00069; pkinase; 1.
 CC PRINTS: PR0019; LEURICHRPT.
 CC PRINTS: PR00109; TYRKINASE.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
 CC Transfaser: Kinase; Serine/threonine-protein kinase; Receptor;
 CC Steroid-binding; ATP-binding; Repeat; Signal; Transmembrane;
 CC Leucine-rich repeat; Glycoprotein; Phosphorylation.
 CC SIGNAL: 1 23 POTENTIAL.
 CC FT CHAIN 24 1196 BRASSINOSTEROID INSENSITIVE 1.
 CC FT TRANSMEM 793 813 POTENTIAL.
 CC FT REPEAT 98 121 LRR 1.
 CC FT REPEAT 122 146 LRR 2.
 CC FT REPEAT 148 169 LRR 3.
 CC FT REPEAT 172 197 LRR 4.
 CC FT REPEAT 199 221 LRR 5.
 CC FT REPEAT 222 244 LRR 6.
 CC FT REPEAT 245 268 LRR 7.
 CC FT REPEAT 269 290 LRR 8.
 CC -----
 CC Query Match 2.2%; Score 9; DB 1; Length 1196;
 CC Best Local Similarity 100.0%; Pred. No. 1.5;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 131 IGSGGFGDV 139
 CC Db 889 IGSGGFGDV 897
 CC -----
 CC RESULT 11
 CC YK10_ARCFU
 CC ID YK10_ARCFU STANDARD; PRT; 232 AA.
 CC AC O28269;
 CC DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF2010.
GN AF2010.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kavelavage A.R., Graham D.B., Kyripides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Geary J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -----
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CC -----
CC EMBL; Z99494; CAB16668.1; --
CC EMBL; AL583924; CAC31098.1; --
CC PIR; T45344; T45344.
CC Leproma; ML2143; --
CC Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
FT TRANSMEM 228 248 POTENTIAL.
FT TRANSMEM 279 299 POTENTIAL.
FT TRANSMEM 303 323 POTENTIAL.
FT TRANSMEM 378 398 POTENTIAL.
FT TRANSMEM 407 427 POTENTIAL.
FT TRANSMEM 448 468 POTENTIAL.
FT TRANSMEM 504 524 POTENTIAL.
FT TRANSMEM 526 546 POTENTIAL.
SQ SEQUENCE 579 AA; B6797F5FA0B22799 CRC64;
Query Match 1.9%; Score 8; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 GLRTRTGS 183
DB 17 GLRTRTGS 24
RESULT 13
BR11 LYCES STANDARD; PRT; 1207 AA.
ID BR11 LYCES STANDARD; PRT; 1207 AA.
AC Q8GQ5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brassinosteroid LRR receptor kinase precursor (EC 2.7.1.37) (tBR11)
DE (Altered brassinolide sensitivity 1) (Systemin receptor SR160).
GN CURL3.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A., AND MUTANT CU3-ABS/ABS1.
RX MEDLINE=22356999; PubMed=12468734;
RA Montoya T., Nomura T., Farrar K., Kaneta T., Yokota T., Bishop G.J.;
RT "Cloning the tomato curl3 gene highlights the putative dual role of
RT the leucine-rich repeat receptor kinase tBR11/SR160 in plant steroid
RT hormone and peptide hormone signaling.";
RL Plant Cell 14:3163-3176(2002).
RN [2]
RP SUBSTRATE BINDING.
RX MEDLINE=22103620; PubMed=12060717;
RA Scheer J.M., Ryan C.A. Jr.;
RT "The systemin receptor SR160 from Lycopersicon peruvianum is a member
RT of the LRR receptor kinase family.";
Query Match 1.9%; Score 8; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 174 ESGLRTRT 181
DB 29 ESGLRTRT 36
RESULT 12
Y876 MYCLE
ID Y876 MYCLE STANDARD; PRT; 579 AA.
AC Q33057;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ML2143.
GN ML2143 OR MLCB57.28C.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigemeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Proc. Natl. Acad. Sci. U.S.A. 99:9585-9590(2002).

-!- FUNCTION: Receptor with a serine/threonine-protein kinase activity. Regulates, in response to brassinosteroid binding, a signaling cascade involved in plant development, including expression of light- and stress-regulated genes, promotion of cell elongation, normal leaf and chloroplast senescence, and flowering. May be involved in a feedback regulation of brassinosteroid biosynthesis. May be also involved in the perception of systemin, a peptide hormone responsible for the systemic activation of defense genes in leaves of wounded plants (By similarity).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.

-!- MISCELLANEOUS: A 68 amino acid island between the 20th and the 21th LRR is essential for the binding of brassinosteroids (By similarity).

-!- MISCELLANEOUS: BR11 is almost identical to SR160, a systemin receptor identified in *Lycopersicon peruvianum*. Competition experiments indicated that brassinosteroid and systemin are probably perceived by different regions of the receptor.

-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

-!- SIMILARITY: Contains 24 leucine-rich (LRR) repeats.

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EMBL: AY179606; AAN85409.1; -
 InterPro: IPR001611; LRR.
 InterPro: IPR007090; LRR plant.
 InterPro: IPR000719; Prot_kinase.
 InterPro: IPR008271; Ser_Thr_pkin_AS.
 InterPro: IPR002290; Ser_Thr_pkinase.
 InterPro: IPR001245; Tyr_pkinase.
 Pfam: PF00560; LRR; 18.
 PRINTS: PR00019; LEURICHPPT.
 PRINTS: PR00103; TYRKINASE.
 ProDom: PD000001; Prot_kinase; 1.
 SMART: SM00220; S_TKc; 1.
 SMART: SM00219; TyrKc; 1.
 PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 Plant defense; transferase; Kinase; Serine/threonine-protein kinase; Receptor; ATP-binding; Steroid-binding; Repeat; Signal; Transmembrane; Leucine-rich repeat; Glycoprotein.

FT SIGNAL 1 34 POTENTIAL
 FT CHAIN 35 1207 BRASSINOSTEROID LRR RECEPTOR KINASE.
 FT TRANSMEM 803 823 POTENTIAL.
 FT REPEAT 80 106 LRR 1.
 FT REPEAT 107 131 LRR 2.
 FT REPEAT 133 158 LRR 3.
 FT REPEAT 159 182 LRR 4.
 FT REPEAT 184 206 LRR 5.
 FT REPEAT 211 235 LRR 6.
 FT REPEAT 237 255 LRR 7.
 FT REPEAT 256 280 LRR 8.
 FT REPEAT 327 307 LRR 9.
 FT REPEAT 327 350 LRR 10.
 FT REPEAT 351 375 LRR 11.
 FT REPEAT 376 399 LRR 12.
 FT REPEAT 400 424 LRR 13.
 FT REPEAT 426 450 LRR 14.
 FT REPEAT 452 474 LRR 15.
 FT REPEAT 475 498 LRR 16.
 FT REPEAT 499 522 LRR 17.
 FT REPEAT 524 546 LRR 18.
 FT REPEAT 547 570 LRR 19.
 FT REPEAT 572 594 LRR 20.

662 686
 REPEAT 687 709
 REPEAT 710 734
 REPEAT 735 759
 REPEAT 888 1163
 FT DOMAIN 894 902
 FT NP_BIND 916 916
 FT BINDING 1014 1014
 FT ACT_SITE 71 78
 FT SITE 771 779
 FT SITE 119 119
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 FT CARBOHYD 196 196
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 FT CARBOHYD 339 339
 FT CARBOHYD 363 363
 FT CARBOHYD 412 412
 FT CARBOHYD 449 449
 FT CARBOHYD 521 521
 FT CARBOHYD 556 556
 FT CARBOHYD 584 584
 FT CARBOHYD 646 646
 FT CARBOHYD 662 662
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 FT CARBOHYD 767 767
 FT MUTAGEN 1012 1012
 SQ SEQUENCE 1207 AA; 131956 MW; 6C370BA048060B7F CRC64;

Query Match 1.9%; Score 8; DB 1; Length 1207;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
 DB 895 GSGGFGDV 902
 |||||

RESULT 14
 BR11_LYCPE STANDARD; PRT; 1207 AA.
 ID BR11_LYCPE
 AC Q8L899;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Systemin receptor SR160 precursor (EC 2.7.1.37) (Brassinosteroid LRR receptor kinase).
 OS *Lycopersicon peruvianum* (Peruvian tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4082;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 301-311; 432-440; 548-554 AND 862-874,
 RP GLYCOSYLATION, AND SUBSTRATE BINDING.
 RX MEDLINE=22103620; PubMed=12060717;
 RA Scheer J.M., Ryan C.A. Jr.;
 RT "The systemin receptor SR160 from *Lycopersicon peruvianum* is a member
 of the LRR receptor kinase family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9585-9590(2002).
 CC -!- FUNCTION: Receptor with a serine/threonine-protein kinase
 CC activity. Involved in the perception of systemin, a peptide
 CC hormone responsible for the systemic activation of defense genes
 CC in leaves of wounded plants. May also regulate, in response to
 CC brassinosteroid binding, a signaling cascade involved in plant
 CC development (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- FTN: Glycosylated.
 CC -!- MISCELLANEOUS: A 68 amino acid island between the 20th and the

21th LRR is essential for the binding of brassinosteroids (By similarity).
-!- MISCELLANEOUS: SR160 is almost identical to BR11, a brassinosteroid receptor identified in Lycopersicon esculentum. Competition experiments indicate that brassinosteroid and systemin are probably perceived by different regions of the receptor.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Contains 24 leucine-rich (LRR) repeats.
CC
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CC
CC EMBL: AY112661; AAM48285.1; --
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 19.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW plant defense; Transferase; Kinase; Serine/threonine-protein kinase;
KW Receptor; ATP-binding; Steroid-binding; Repeat; Signal; Transmembrane;
KW Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 1207 SYSTEMIN RECEPTOR SR160.
FT TRANSMEM 803 823 POTENTIAL.
FT REPEAT 80 106 LRR 1.
FT REPEAT 107 131 LRR 2.
FT REPEAT 133 158 LRR 3.
FT REPEAT 159 182 LRR 4.
FT REPEAT 184 206 LRR 5.
FT REPEAT 211 235 LRR 6.
FT REPEAT 237 255 LRR 7.
FT REPEAT 256 280 LRR 8.
FT REPEAT 282 307 LRR 9.
FT REPEAT 327 350 LRR 10.
FT REPEAT 351 375 LRR 11.
FT REPEAT 376 399 LRR 12.
FT REPEAT 400 424 LRR 13.
FT REPEAT 426 450 LRR 14.
FT REPEAT 452 474 LRR 15.
FT REPEAT 475 498 LRR 16.
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FT REPEAT 887 910 LRR 33.
FT REPEAT 911 934 LRR 34.
FT REPEAT 935 958 LRR 35.
FT REPEAT 959 982 LRR 36.
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FT REPEAT 8615 8638 LRR 355.
FT REPEAT 8639 8662 LRR 356.
FT REPEAT 8663 8686 LRR 357.
FT REPEAT 8687 8710 LRR 358.
FT REPEAT 8711 8734 LRR 359.
FT REPEAT 8735 8758 LRR 360.
FT REPEAT 8759 8782 LRR 361.
FT REPEAT 8783 8806 LRR 362.
FT REPEAT 8807 8830 LRR 363.
FT REPEAT 8831 8854 LRR 364.
FT REPEAT 8855 8878 LRR 365.
FT REPEAT 8879 8902 LRR 366.
FT REPEAT 8903 8926 LRR 367.
FT REPEAT 8927 8950 LRR 368.
FT REPEAT 8951 8974 LRR 369.
FT REPEAT 8975 8998 LRR 370.
FT REPEAT 8999 9022 LRR 371.
FT REPEAT 9023 9046 LRR 372.
FT REPEAT 9047 9070 LRR 373.
FT REPEAT 9071 9094 LRR 374.
FT REPEAT 9095 9118 LRR 375.
FT REPEAT 9119 9142 LRR 376.
FT REPEAT 9143 9166 LRR 377.
FT REPEAT 9167 9190 LRR 378.
FT REPEAT 9191 9214 LRR 379.
FT REPEAT 9215 9238 LRR 380.
FT REPEAT 9239 9262 LRR 381.
FT REPEAT 9263 9286 LRR 382.
FT REPEAT 9287 9310 LRR 383.
FT REPEAT 9311 9334 LRR 384.
FT REPEAT 9335 9358 LRR 385.
FT REPEAT 9359 9382 LRR 386.
FT REPEAT 9383 9406 LRR 387.
FT REPEAT 9407 9430 LRR 388.
FT REPEAT 9431 9454 LRR 389.
FT REPEAT 9455 9478 LRR 390.
FT REPEAT 9479 9502 LRR 391.
FT REPEAT 9503 9526 LRR 392.
FT REPEAT 9527 9550 LRR 393.
FT REPEAT 9551 9574 LRR 394.
FT REPEAT 9575 9598 LRR 395.
FT REPEAT 9599 9622 LRR 396.
FT REPEAT 9623 9646 LRR 397.
FT REPEAT 9647 9670 LRR 398.
FT REPEAT 9671 9694 LRR 399.
FT REPEAT 9695 9718 LRR 400.
FT REPEAT 9719 9742 LRR 401.
FT REPEAT 9743 9766 LRR 402.
FT REPEAT 9767 9790 LRR 403.
FT REPEAT 9791 9814 LRR 404.
FT REPEAT 9815 9838 LRR 405.
FT REPEAT 9839 9862 LRR 406.
FT REPEAT 9863 9886 LRR 407.
FT REPEAT 9887 9910 LRR 408.
FT REPEAT 9911 9934 LRR 409.
FT REPEAT 9935 9958 LRR 410.
FT REPEAT 9959 9982 LRR 411.
FT REPEAT 9983 10006 LRR 412.
FT REPEAT 10007 10030 LRR 413.
FT REPEAT 10031 10054 LRR 414.
FT REPEAT 10055 10078 LRR 415.
FT REPEAT 10079 10102 LRR 416.
FT REPEAT 10103 10126 LRR 417.
FT REPEAT 10127 10150 LRR 418.
FT REPEAT 10151 10174 LRR 419.
FT REPEAT 10175 10198 LRR 420.
FT REPEAT 10199 10222 LRR 421.
FT REPEAT 10223 10246 LRR 422.
FT REPEAT 10247 10270 LRR 423.
FT REPEAT 10271 10294 LRR 424.
FT REPEAT 10295 10318 LRR 425.
FT REPEAT 10319 10342 LRR 426.
FT REPEAT 10343 10366 LRR 427.
FT REPEAT 10367 10390 LRR 428.
FT REPEAT 10391 10414 LRR 429.
FT REPEAT 10415 10438 LRR 430.
FT REPEAT 10439 10462 LRR 431.
FT REPEAT 10463 10486 LRR 432.
FT REPEAT 10487 10510 LRR 433.
FT REPEAT 10511 10534 LRR 434.
FT REPEAT 10535 10558 LRR 435.
FT REPEAT 10559 10582 LRR 436.
FT REPEAT 10583 10606 LRR 437.
FT REPEAT 10607 10630 LRR 438.
FT REPEAT 10631 10654 LRR 439.
FT REPEAT 10655 10678 LRR 440.
FT REPEAT 10679 10702 LRR 441.
FT REPEAT 10703 10726 LRR 442.
FT REPEAT 10727 10750 LRR 443.
FT REPEAT 10751 10774 LRR 444.
FT REPEAT 10775 10798 LRR 445.
FT REPEAT 10799 10822 LRR 446.
FT REPEAT 10823 10846 LRR 447.
FT REPEAT 10847 10870 LRR 448.
FT REPEAT 10871 10894 LRR 449.
FT REPEAT 10895 10918 LRR 450.
FT REPEAT 10919 10942 LRR 451.
FT REPEAT 10943 10966 LRR 452.
FT REPEAT 10967 10990 LRR 453.
FT REPEAT 10991 11014 LRR 454.
FT REPEAT 11015 11038 LRR 455.
FT REPEAT 11039 11062 LRR 456.
FT REPEAT 11063 11086 LRR 457.
FT REPEAT 11087 11110 LRR 458.
FT REPEAT 11111 11134 LRR 459.
FT REPEAT 11135 11158 LRR 460.
FT REPEAT 11159 11182 LRR 461.
FT REPEAT 11183 11206 LRR 462.
FT REPEAT 11207 11230 LRR 463.
FT REPEAT 11231 11254 LRR 464.
FT REPEAT 11255 11278 LRR 465.
FT REPEAT 11279 11302 LRR 466.
FT REPEAT 11303 11326 LRR 467.
FT REPEAT 11327 11350 LRR 468.
FT REPEAT 11351 11374 LRR 469.
FT REPEAT 11375 11398 LRR 470.
FT REPEAT 11399 11422 LRR 471.
FT REPEAT 11423 11446 LRR 472.
FT REPEAT 11447 11470 LRR 473.
FT REPEAT 11471 11494 LRR 474.
FT REPEAT 11495 11518 LRR 475.
FT REPEAT 11519 11542 LRR 476.
FT REPEAT 11543 11566 LRR 477.
FT REPEAT 11567 11590 LRR 478.
FT REPEAT 11591 11614 LRR 479.
FT REPEAT 11615 11638 LRR 480.
FT REPEAT 11639 11662 LRR 481.
FT REPEAT 11663 11686 LRR 482.
FT REPEAT 11687 11710 LRR 483.
FT REPEAT 11711 11734 LRR 484.
FT REPEAT 11735 11758 LRR 485.
FT REPEAT 11759 11782 LRR 486.
FT REPEAT 11783 11806 LRR 487.
FT REPEAT 11807 11830 LRR 488.
FT REPEAT 11831 11854 LRR 489.
FT REPEAT 11855 11878 LRR 490.
FT REPEAT 11879 11902 LRR 491.
FT REPEAT 11903 11926 LRR 492.
FT REPEAT 11927 11950 LRR 493.
FT REPEAT 11951 11974 LRR 494.
FT REPEAT 11975 12000 LRR 495.
FT REPEAT 12001 12024 LRR 496.
FT REPEAT 12025 12048 LRR 497.
FT REPEAT 12049 12072 LRR 498.
FT REPEAT 12073 12096 LRR 499.
FT REPEAT 12097 12120 LRR 500.
FT REPEAT 12121 12144 LRR 501.
FT REPEAT 12145 12168 LRR 502.
FT REPEAT 12169 12192 LRR 503.
FT REPEAT 12193 12216 LRR 504.
FT REPEAT 12217 12240 LRR 505.
FT REPEAT 12241 12264 LRR 506.
FT REPEAT 12265 12288 LRR 507.
FT REPEAT 12289 12312 LRR 508.
FT REPEAT 12313 12336 LRR 509.
FT REPEAT 12337 12360 LRR 510.
FT REPEAT 12361 12384 LRR 511.
FT REPEAT 12385 12408 LRR 512.
FT REPEAT 12409 12432 LRR 513.
FT REPEAT 12433 12456 LRR 514.
FT REPEAT 12457 12480 LRR 515.
FT REPEAT 12481 12504 LRR 516.
FT REPEAT 12505 12528 LRR 517.
FT REPEAT 12529 12552 LRR 518.
FT REPEAT 12553 12576 LRR 519.
FT REPEAT 12577 12600 LRR 520.
FT REPEAT 12601 126

"The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";
 Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.
 -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + RNA(N).
 -!- SUBUNIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1 beta chain.
 -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
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 EMBL; AE001593; AAD18235.1; -
 EMBL; AE002228; AAF38501.1; ALT_INIT.
 EMBL; AP002545; BAA98292.1; -
 EMBL; AE017157; AAF98015.1; -
 DR PIR; B86501; B86501.
 DR PIR; E72122; E72122.
 DR HSP; O9KWU6; IHQM.
 DR TIGR; CP0693; -
 DR InterPro; IPR000722; RNA_pol_A.
 DR InterPro; IPR007080; RNA_pol_Rpbl_1.
 DR InterPro; IPR007066; RNA_pol_Rpbl_3.
 DR InterPro; IPR007083; RNA_pol_Rpbl_4.
 DR InterPro; IPR007081; RNA_pol_Rpbl_5.
 DR InterPro; IPR006592; RNA_pol_A_N.
 DR Pfam; PF04997; RNA_pol_Rpbl_1; 1.
 DR Pfam; PF00623; RNA_pol_Rpbl_2; 1.
 DR Pfam; PF04983; RNA_pol_Rpbl_3; 1.
 DR Pfam; PF05000; RNA_pol_Rpbl_4; 1.
 DR Pfam; PF04998; RNA_pol_Rpbl_5; 1.
 DR SMART; SM00663; RPOLA_N; 1.
 KW Transferrase, DNA-directed RNA polymerase; Transcription;
 KW Complete proteome.
 FT CONFLICT 1031 1031 A -> G (IN REF. 1).
 SQ SEQUENCE 1393 AA; 154900 MW; E0734FF236C6FDE8 CRC64;
 Query Match 1.9%; Score 8; DB 1; Length 1393;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 377 SEDLQSL 384
 Db 194 SEDLQSL 201
 |||||
 RESULT 16
 GCSE MYCLE STANDARD; PRT; 132 AA.
 AC Q32920;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2001 (Rel. 40, Last sequence update)
 DE Glycine cleavage system H protein.
 GN GCVH OR ML2077 OR MLCB1788.37C.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagsels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
 "Massive gene decay in the leprosy bacillus.";
 Nature 409:1007-1011(2001).
 -!- FUNCTION: The glycine cleavage system catalyzes the degradation of glycine. The H protein shuttles the methylamine group of glycine from the P protein to the T protein (By similarity).
 -!- COFACTOR: The H chain contains a covalently-bound lipoyl cofactor (By similarity).
 -!- SUBUNIT: The glycine cleavage system is composed of four proteins: P, T, L and H (By similarity).
 -!- SIMILARITY: Belongs to the gcvH family.
 -!- SIMILARITY: Contains 1 lipoyl-binding domain.
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 EMBL; AL008609; CRA15469.1; -
 EMBL; AL583924; CAC31032.1; -
 DR PIR; T44759; T44759.
 DR HSP; P16048; IHTP.
 DR Leproma; ML2077; -
 DR HAMAP; MF 00272; -; 1.
 DR InterPro; IPR002930; GCV_H.
 DR InterPro; IPR003016; Lipoyl_BS.
 DR Pfam; PF01597; GCV_H; 1.
 DR TIGRFAMS; TIGR00527; gcvH; 1.
 DR PROSITE; PS00189; LIPOYL; 1.
 KW Lipoyl; Complete proteome.
 FT BINDING 65 65 LIPOYL (BY SIMILARITY).
 SQ SEQUENCE 132 AA; 14070 MW; 2DBF05D69BA1C6AA CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 138 DVGAL 144
 Db 109 DVGAL 115
 |||||
 RESULT 17
 PTH CHLPN STANDARD; PRT; 180 AA.
 AC Q9Z6V6; Q9JQCC;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH).
 GN PTH OR CPN0950 OR CP0909 OR CP0987.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RX Geng M.M., Schuhmacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The natural substrate for this enzyme may be peptidyl-
CC tRNAs which drop off the ribosome during protein synthesis (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: N-substituted aminoacyl-tRNA + H(2)O = N-
CC substituted amino acid + tRNA.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the PTH family.
CC
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CC
CC EMBL; AA01675; AAD19088.1; -;
CC EMBL; AE002250; AAF38694.1; -;
CC EMBL; AP002548; BAA99158.1; -;
CC EMBL; AE017160; AAP98916.1; -;
CC PIR; D86609; D86609.
CC F01; E72014; E72014.
CC HSP; F23932; 2PTH.
CC TIGR; CP0909; -;
CC HAMAP; MF_00083; -; 1.
CC InterPro; IPR001328; Pept tRNA hydro.
CC Pfam; PF01195; Pept tRNA hydro; 1.
CC ProDom; PD005324; Pept tRNA hydro; 1.
CC PROSITE; PS01195; PEPT_TRNA_HYDROL_1; 1.
CC PROSITE; PS01196; PEPT_TRNA_HYDROL_2; 1.
CC Hydrolase; Complete proteome.
KW SEQUENCE 180 AA; 19645 MW; 12A7FA7A0F62564A CRC64;
Query Match 1.7%; Score 7; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 RLVEELQ 21
DB 29 RLVEELQ 35
RESULT 18
HNK2_XENLA

ID HNK2_XENLA STANDARD; PRT; 196 AA.
AC P42587;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein XENK-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic head;
RX MEDLINE=93387212; PubMed=8104140;
RA Saha M.S., Michel R.B., Guldung K.M., Grainger R.M.;
RT "A Xenopus homeobox gene defines dorsal-ventral domains in the
RT developing brain.";
RL Development 118:193-202(1993).
CC -!- FUNCTION: Defines dorsal-ventral domains in developing brain. May
CC play a role in defining positional information along the
CC anterior-posterior (a/p) axis and the dorsal-ventral (d/v) axis of
CC the developing nervous system. May be involved in determining
CC positional or boundary information rather than determining a given
CC cell type.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Forebrain and midbrain.
CC -!- DEVELOPMENTAL STAGE: Is first detectable at the neural plate stage
CC (stage 14). Levels gradually increase during later neurula stages,
CC and becomes fairly constant throughout tailbud and hatching stages,
CC before declining at late swimming tadpole stages.
CC -!- SIMILARITY: Belongs to the NK-2 homeobox family.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC
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CC
CC EMBL; L10327; AAA72342.1; -;
CC EMBL; S65507; AAB28271.2; -;
CC HSP; P22808; LNK3.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT DNA_BIND 69 128 HOMEBOX.
SQ SEQUENCE 196 AA; 22809 MW; F5A0657470C1031B CRC64;
Query Match 1.7%; Score 7; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 VLRPPIR 116
DB 31 VLRPPIR 37
RESULT 19
GIDB_RHILO STANDARD; PRT; 210 AA.
ID GIDB_RHILO
AC Q98D22;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyltransferase gidB (EC 2.1.1.-) (Glucose inhibited division

DE protein B).
 GN GIDB OR ML14481.
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Phyllobacteriaceae; Mesorhizobium.
 OK NCBI_TaxID=381;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shampo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 CC -!- FUNCTION: Probable S-adenosyl-L-methionine dependent
 CC methyltransferase specific for a sterol and/or lipid substrate (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the gidB family.
 CC
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 CC
 CC EMBL; AP003004; BAB51128.1; -.
 DR HAMAP; MF 00074; -; 1.
 DR InterPro; IPR003682; GidB.
 DR Pfam; PF02527; GidB; 1.
 DR ProDom; PD004441; GidB; 1.
 DR TIGRFAMs; TIGR00138; gidB; 1.
 DR Transferase; Methyltransferase; Complete proteome.
 KW SEQUENCE 210 AA; 23107 MW; F798AB0C33329AB CRC64;
 SQ
 Query Match 1.7%; Score 7; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 129 VDIGSGG 135
 Db 71 VDIGSGG 77
 RESULT 20
 RS3_RALSO STANDARD; PRT; 264 AA.
 AC Q8XV18;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S3
 GN RSCC OR RSC3013 OR RSC01076.
 OS Ralstonia solanacearum (pseudomonas solanacearum).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Burkholderiaceae; Ralstonia.
 OK NCBI_TaxID=305;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguer P., Tiebaut P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).
 CC -!- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
 CC in the 70S ribosome, positioning it for translation (By
 CC similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
 CC with proteins S10 and S14 (By similarity).
 CC -!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
 CC -!- SIMILARITY: Contains 1 KH type-2 domain.
 CC
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 CC
 CC EMBL; AL646073; CAD16722.1; -.
 DR HAMAP; MF 01309; -; 1.
 DR InterPro; IPR004087; KH dom.
 DR InterPro; IPR009019; KH prok.
 DR InterPro; IPR004044; KH TYPE 2.
 DR InterPro; IPR001351; Ribosomal_S3_C.
 DR InterPro; IPR008282; Ribosomal_S3_N.
 DR InterPro; IPR005704; S3_bact.
 DR Pfam; PF00013; KH; 1.
 DR Pfam; PF00189; Ribosomal_S3_C; 1.
 DR Pfam; PF00417; Ribosomal_S3_N; 1.
 DR SMART; SM00322; KH; 1.
 DR TIGRFAMs; TIGR01009; rpsc_bact; 1.
 DR PROSITE; PS00823; KH TYPE 2; 1.
 DR PROSITE; PS00548; RIBOSOMAL_S3; 1.
 KW Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
 FT DOMAIN 39 107 KH TYPE-2.
 SQ SEQUENCE 264 AA; 29738 MW; 72BBCACF1EC2DD3E CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 114 EIRKPEV 120
 Db 105 EIRKPEV 111
 RESULT 21
 NHS_STRAS
 ID NHS_STRAS STANDARD; PRT; 274 AA.
 AC P52391;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 23S rRNA methyltransferase (EC 2.1.1.-) (23S rRNA methylase).
 GN NHS.
 OS Streptomyces actuosus.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycineae; Streptomycetaceae; Streptomyces.
 OK NCBI_TaxID=1885;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25421;
 RX MEDLINE=90382703; PubMed=2401410;
 RA Li Y., Dosch D.C., Strohl W.R., Floss H.G.;
 RT "Nucleotide sequence and transcriptional analysis of the nosiheptide-
 RT resistance gene from Streptomyces actuosus.";
 RL Gene 91:9-17(1990).
 CC -!- FUNCTION: CONFERS RESISTANCE TO ANTIBIOTIC NOSIHEPTIDE.
 CC -!- SIMILARITY: TO S.AZUREUS TSR.
 CC
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CC -----

DR EMBL; U75434; AAB17875.1; -.

DR PIR; JQ0686; JQ0686.

DR InterPro; IPR001537; SpoU methylase.

DR InterPro; IPR006795; TSNR_N.

DR Pfam; PF00588; SpoU methylase; 1.

DR Pfam; PF04705; TSNR_N; 1.

DR ProDom; PD001243; SpoU methylase; 1.

DR Antibiotic resistance; Transferase; Methyltransferase.

CC SEQUENCE 274 AA; 29183 MW; 9FA2CL1B2E8BF24D CRC64;

Query Match 1.7%; Score 7; DB 1; Length 274;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADRELLR 10

DB 156 ADRELLR 162

RESULT 22

SDSB_PSES9 STANDARD; PRT; 306 AA.

AC P52686;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE SDS degradation transcriptional activation protein.

GN SDSB.

OS Pseudomonas sp. (strain ATCC 19151).

OC Bacteria; Proteobacteria.

OX NCBI_TaxID=315;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92267380; PubMed=1587481;

RA Davison J., Brunel F., Phanopoulos A., Prozzi D., Terpstra P.;

RT "Cloning and sequencing of Pseudomonas genes determining sodium

RT dodecyl sulfate biodegradation.";

RL Gene 114:19-24(1992).

CC -!- FUNCTION: ACTIVATES THE TRANSCRIPTION OF THE SDSA GENE FOR

CC -!- SODIUM DODECYL SULFATE (SDS) DEGRADATION.

CC -!- SIMILARITY: Contains 1 HTH lyser-type DNA-binding domain.

CC -----

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CC -----

DR EMBL; M86744; AAA25988.1; -.

DR InterPro; IPR000847; HTH_LysR.

DR InterPro; IPR005119; LysR_subst.

DR Pfam; PF00126; HTH_1; 1.

DR Pfam; PF03466; LysR_substrate; 1.

DR PROSITE; PS00931; HTH_LYSR; 1.

KW Transcription regulation; DNA-binding; Activator.

FT DOMAIN 1 59 HTH_LYSR-TYPE.

FT DNA_BIND 19 38 H-T-H MOTIF (POTENTIAL).

CC SEQUENCE 306 AA; 32955 MW; BE1A6EACF3FE24FA CRC64;

Query Match 1.7%; Score 7; DB 1; Length 306;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELA 220

DB 256 LALLELA 262

RESULT 23

G3P_THEVO STANDARD; PRT; 338 AA.

AC Q97BU8;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.59) (GAPDH)

DE (NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase).

GN GAP OR TV0457 OR TVG0444310.

OS Thermoplasma volcanium.

OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

OC Thermoplasmataceae; Thermoplasma.

OX NCBI_TaxID=50339;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=GSS1 / DSM 4299 / JCM 9571;

RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

RA Nunoshiba T., Yamamoto Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,

RA "Archaeal adaptation to higher temperatures revealed by genomic

RT sequence of Thermoplasma volcanium."

RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +

CC NAD(P)(+) = 3-phospho-D-glyceroyl phosphate + NAD(P)H.

CC -!- PATHWAY: Second phase of glycolysis; first step.

CC -!- SUBUNIT: Homotetramer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate

CC dehydrogenase family.

CC -----

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CC -----

DR EMBL; AP000992; BAB59599.1; -.

DR HAMAP; MF_00559; -; 1.

DR InterPro; IPR000173; GAP_dhdhydrogenase.

DR InterPro; IPR006436; GAPDH-II_archae.

DR Pfam; PF00044; gpdh; 1.

DR Pfam; PF02800; gpdh_C; 1.

DR ProDom; PD007761; GAPDH-II_archae; 1.

DR TIGRFAMs; TIGR01546; GAPDH-II_archae; 1.

DR PROSITE; PS00711; GAPDH; 1.

DR Glycolysis; Oxidoreductase;

FT BINDING 139 139 NAD; NADP; Complete proteome.

FT BINDING 139 139 GLYCERALDEHYDE 3-PHOSPHATE (BY

FT BINDING 139 139 SIMILARITY).

CC SEQUENCE 338 AA; 37374 MW; C9BD53DFD4722F34 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 338;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 RVANAVS 392

DB 15 RVANAVS 21

RESULT 24

TRPD_AERPE

ID TRPD_AERPE STANDARD; PRT; 345 AA.

AC Q9Y872;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Anthranilate phosphoribosyltransferase (EC 2.4.2.18).

FT TRPD OR APE2551.

```

OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosylidiphosphate =
CC N-5'-phosphoribosyl-anthranilate + diphosphate.
CC -!- PATHWAY: Tryptophan biosynthesis; second step.
CC -!- SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase
CC family.
CC
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CC
CC EMBL; AP000064; BAA81568.1; -.
CC PIR; H72488; H72488.
CC DR HAMAP; MF 00211; -.
CC DR InterPro; IPR005940; Ant_phospho_trans.
CC DR InterPro; IPR000312; Glyco_trans_3.
CC DR Pfam; PF02885; Glycos_trans_3N; 1.
CC DR Pfam; PF00591; Glycos_transf_3; 1.
CC DR Pfam; PD001864; Glyco_trans_3; 1.
CC DR TIGRFAMs; TIGR01245; trpD; 1.
CC DR TIGRFAMs; TIGR01245; trpD; 1.
CC KW Tryptophan biosynthesis; Transferase; Glycosyltransferase;
CC Complete proteome.
CC FT DOMAIN 299 305 POLY-ALA.
CC ST SEQUENCE 345 AA; 36449 MW; 5CBF8E8B4EAC2B CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 345;
CC Best Local Similarity 100.0%; Pred.No.55;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 385 LRVANAV 391
CC Db 270 LRVANAV 276
CC
CC RESULT 25
CC TRUD_SALTY
CC ID TRUD_SALTY STANDARD; PRT; 349 AA.
CC AC Q8Z473;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE tRNA pseudouridine synthase D (EC 4.2.1.70) (Pseudouridylylate synthase)
CC DE (Uracil hydrolyase).
CC GN TRUD OR STV3053 OR T2829.
CC OS Salmonella typhi.
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Salmonella.
CC OX NCBI_TaxID=601;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=CT18;
CC RX MEDLINE=21534947; PubMed=11677608;
CC RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,

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RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsis K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Responsible for synthesis of pseudouridine from
CC uracil-13 in transfer RNAs (By similarity).
CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
CC 5'-phosphate + H(2)O.
CC -!- SIMILARITY: Belongs to the pseudouridine synthase truD family.
CC
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CC
CC EMBL; AL627276; CAD06034.1; -.
CC EMBL; AE016843; AA070386.1; -.
CC DR HAMAP; MF_01082; -.
CC DR InterPro; IPR001656; UPF0024.
CC DR Pfam; PF01142; UPF0024; 1.
CC DR TIGRFAMs; TIGR00094; TIGR00094; 1.
CC DR PROSITE; PS01268; UPF0024; 1.
CC KW tRNA processing; Lyase; Complete proteome.
CC FT ACT_SITE 80 80 BY SIMILARITY.
CC ST SEQUENCE 349 AA; 39361 MW; 548A1BA51A8F3E7A CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 349;
CC Best Local Similarity 100.0%; Pred.No.55;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 380 LOSLLLR 386
CC Db 285 LOSLLLR 291
CC
CC RESULT 26
CC TRUD_SALTY
CC ID TRUD_SALTY STANDARD; PRT; 349 AA.
CC AC Q8ZMF8;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE tRNA pseudouridine synthase D (EC 4.2.1.70) (Pseudouridylylate synthase)
CC DE (Uracil hydrolyase).
CC GN TRUD OR STM2928.
CC OS Salmonella typhimurium.
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Salmonella.
CC OX NCBI_TaxID=602;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
CC RX MEDLINE=21534948; PubMed=11677609;
CC RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
CC Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

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RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT L12.",
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: Responsible for synthesis of pseudouridine from
 CC uracil-13 in transfer RNAs (By similarity).
 CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
 CC 5'-phosphate + H(2)O.
 CC -!- SIMILARITY: Belongs to the pseudouridine synthase truD family.
 CC
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 CC
 CC EMBL; AE008833; AAL21808.1; -
 CC STyGene; SG????; truD.
 CC HAMAP; MF_01082; -; 1.
 CC InterPro; IPR001656; UPF0024.
 CC Pfam; PF01142; UPF0024; 1..000094; 1.
 CC TIGRFAMs; TIGR00094; TIGR00094; 1.
 CC PROSITE; PS01268; UPF0024; 1.
 CC TRNA processing; Lyase; Complete proteome.
 CC ACT SITE 80 80 BY SIMILARITY.
 CC SEQUENCE 349 AA; 39332 MW; 5357437747CDSA51 CRC64;
 CC
 CC Query Match 1.7%; Score 7; DB 1; Length 349;
 CC Best Local Similarity 100.0%; Pred.No. 55;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 380 LQSLLLR 386
 CC Db 285 LQSLLLR 291
 CC
 CC RESULT 27
 CC ID RAD1_YEAST STANDARD; PRT; 401 AA.
 CC AC P48581;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
 CC DE DNA damage checkpoint control protein RAD17.
 CC GN RAD17 OR YOR368W.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC OX NCBI_TaxID=4932;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=96211370; PubMed=8649984;
 CC RA Siede W., Dianova I., Nussbaumer G., Portillo V., Rodriguez R.,
 CC Nunes E., Friedberg E.C.;
 CC RT "Cloning and characterization of RAD17, a gene controlling cell cycle
 CC responses to DNA damage in *Saccharomyces cerevisiae*.";
 CC RL Nucleic Acids Res. 24:1669-1675(1996).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RA Lydall D., Weinert T.;
 CC RN Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC RP SEQUENCE FROM N.A.
 CC RA Delius H., Hebling U., Hofmann B.;
 CC RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Putative exonuclease involved in DNA damage checkpoint
 CC control.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: SOME, TO S.POMBE RAD1 AND TO U.MAYDIS REC1.

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 CC
 CC EMBL; U37460; AAA80545.1; -
 CC DR EMBL; U30796; AAA93250.1; -
 CC DR EMBL; Z75276; CAA99699.1; -
 CC DR PIR; S59670; S59670.
 CC Germonline; 143956; -
 CC SGP; S0005895; RAD17.
 CC GO; GO:0005634; C:nucleus; IPI.
 CC GO; GO:0000077; P:DNA damage response, signal transduction re. .; IMP.
 CC GO; GO:0007131; P:meiotic recombination; IMP.
 CC DR InterPro; IPR003021; Rad1_Recl.
 CC DR Pfam; PF02144; Rad1; 1.
 CC DR PRINTS; PR01245; RAD1REC1.
 CC KW DNA damage; DNA repair; Hydrolase; Exonuclease; Nuclear protein.
 CC FT VARIANT 128 128 E -> K (IN RAD17-1; UV-SENSITIVE).
 CC SQ SEQUENCE 401 AA; 45579 MW; BFF7074676C483C9 CRC64;
 CC
 CC Query Match 1.7%; Score 7; DB 1; Length 401;
 CC Best Local Similarity 100.0%; Pred.No. 63;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 29 LLSRELF 35
 CC Db 61 LLSRELF 67
 CC
 CC RESULT 28
 CC ID YBR3_YEAST STANDARD; PRT; 404 AA.
 CC AC P38083;
 CC DT 01-OCT-1994 (Rel. 30, Created)
 CC DT 01-OCT-1994 (Rel. 30, Last sequence update)
 CC DT 01-NOV-1995 (Rel. 32, Last annotation update)
 CC DE Hypothetical 46.4 kDa protein in ORC2-TIP1 intergenic region.
 CC GN YBR063C OR YBR0610.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC OX NCBI_TaxID=4932;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=S288c;
 CC RA Domdey H., Gassenhuber H., Obermaier B., Piravandi E.;
 CC RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC
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 CC
 CC EMBL; Z35932; CAA85006.1; -
 CC DR EMBL; Z45923; S45923.
 CC DR Germonline; 138606; -
 CC SGP; S000267; YBR063C.
 CC KW Hypothetical protein; Transmembrane.
 CC FT TRANSMEM 35 55 POTENTIAL.
 CC FT TRANSMEM 92 112
 CC SQ SEQUENCE 404 AA; 46444 MW; B2CC066A6E0A0670 CRC64;
 CC
 CC Query Match 1.7%; Score 7; DB 1; Length 404;
 CC Best Local Similarity 100.0%; Pred.No. 63;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 307 SPGSNPE 313
DB 215 SPGSNPE 221
|||||
|||||

RESULT 29
BACA RHIME STANDARD; PRT; 420 AA.
ID BAC120;
AC Q09120;
DT 01-OCT-1994 (Rel. 30, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteroid development protein bacA.
GN BACA OR RB1125 OR SMB20999.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=93339575; PubMed=8393417;
RA Glazebrook J., Ichige A., Walker G.C.;
RA "A Rhizobium meliloti homolog of the Escherichia coli peptide-
RT antibiotic transport protein SbmA is essential for bacteroid
RT development";
RL Genes Dev. 7:1485-1497 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
RA Golding B., Puhler A.;
RA "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
CC -!- FUNCTION: FUNCTIONS IN THE TRANSPORT OF MOLECULES, POSSIBLY
CC PEPTIDES, ACROSS THE INNER MEMBRANE. IS ESSENTIAL FOR BACTEROID
CC DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- TISSUE SPECIFICITY: NODULES.
CC -!- SIMILARITY: STRONG. TO E.COLI SBMA.
CC
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CC
CC EMBL; X73522; CAA51918.1; -.
CC DR EMBL; AL603646; CAC49525.1; -.
CC DR F1R; A47649; A47649.
CC DR F1R; E95982; E95982.
KW Transport; Transmembrane; Inner membrane; Plasmid; Complete proteome.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 61 81 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 247 267 POTENTIAL.
FT TRANSMEM 336 356 POTENTIAL.
FT TRANSMEM 128 128 A -> P (IN REF. 1).
SQ SEQUENCE 420 AA; 47848 MW; 548496A86AD1D0FE CRC64;

Query Match 1.7%; Score 7; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31
RECA TROWT
ID RECA TROWT STANDARD; PRT; 437 AA.
AC Q83MS9; Q83NC5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

QY 263 IVNIENG 269
DB 240 IVNIENG 246
|||||
|||||

Query Match 1.7%; Score 7; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30
LIP7 CANAL STANDARD; PRT; 426 AA.
ID LIP7 CANAL
AC Q9P4E7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase 7 precursor (EC 3.1.1.3).
GN LIP7.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RC STRAIN=SC5314;
RX MEDLINE=21014758; PubMed=11131027;
RA Hube B., Stehr E., Bossenz M., Mazur A., Kretschmar M., Schaefer W.;
RA "Secreted lipases of Candida albicans: cloning, characterisation and
RT expression analysis of a new gene family with at least ten members.";
RL Arch. Microbiol. 174:362-374 (2000).
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC
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CC
CC EMBL; AF191320; AAF79928.1; -.
CC DR InterPro; IPR005152; LIP.
CC DR Pfam; PF03583; LIP; 1.
KW Lipid degradation; Hydrolase; Signal; Glycoprotein; Multigene family.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 426 LIPASE 7.
FT ACT_SITE 190 190 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 321 321 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 426 AA; 47854 MW; 2DBBABC4CBCC6A85 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 IVNIENG 269
DB 240 IVNIENG 246
|||||
|||||

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RecA protein (Recombinase A).
GN RECA OR TW611 OR TW628.
OS Tropheryma whipplei (strain Twist) (Whipple's bacillus), and
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267, 218496;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Twist;
RC MEDLINE=22784088; PubMed=12902375;
RA Raoult D., Ogata H., Audic S., Robert C., Sühre K., Drancourt M.,
RA Claverie J.-M.;
RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
RT reduced genome.";
RL Genome Res. 13:1800-1809 (2003).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Tw08/27;
RC MEDLINE=22495039; PubMed=12606174;
RA Bentley S.D., Maitwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Relman D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
RT bacterium Tropheryma whipplei.";
RL Lancet 361:637-644 (2003).
CC -!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of
CC single-stranded DNA, the ATP-dependent uptake of single-stranded
CC DNA by duplex DNA, and the ATP-dependent hybridization of
CC homologous single-stranded DNAs. It interacts with lexA causing
CC its activation and leading to its autocatalytic cleavage (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the recA family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC -----
DR EMBL; AE016852; AAO44708.1; ALT INIT.
DR EMBL; BX251412; CAD67292.1; -.
DR HAMAP; MF_00268; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001553; RecA.
DR Pfam; PF00154; recA; 1.
DR PRINTS; PR00142; RECA.
DR ProDom; PD000229; RECA; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00321; RECA_1; 1.
DR PROSITE; PS01621; RECA_2; 1.
DR PROSITE; PS01623; RECA_3; 1.
DR DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
KW Complete proteome.
FT NP BIND 69 76 ATP (BY SIMILARITY).
SQ SEQUENCE 437 AA; 46450 MW; 969186B5C5F390D8 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 358 KSGSWYV 364
Db 289 KSGSWYV 295
RESULT 32
IFR2_HUMAN
ID IFR2_HUMAN STANDARD; PRT; 442 AA.
AC Q12894;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interferon-related developmental regulator 2 (SKMCL5 protein).
GN IFRD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP Dante M., Wamsley P.;
RC Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney, Muscle, and Placenta;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN SEQUENCE OF 2-442 FROM N.A.
RP TISSUE=Skeletal muscle;
RC MEDLINE=97203201; PubMed=9050919;
RA Latif F., Duh F.-M., Bader S., Sekido Y., Li H., Geil L., Zbar B.,
RA Minna J.D., Lerman M.I.;
RT "The human homolog of the rodent immediate early response genes, PC4
RT and TIS7, resides in the lung cancer tumor suppressor gene region on
RT chromosome 3p21.";
RL Hum. Genet. 99:334-341 (1997).
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -!- SIMILARITY: Belongs to the IFRD family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC -----
DR EMBL; U73167; AAC02728.1; -.
DR EMBL; BC001676; AAH01676.1; -.
DR EMBL; BC007265; AAH07265.1; -.
DR EMBL; BC007437; AAH07437.1; -.
DR EMBL; U09585; AAC16924.1; -.
DR Genew; HGNC:5457; IFRD2.
DR MIM; 602725; -.
DR GO; GO:0030154; P:cell differentiation; ISS.
DR GO; GO:0008283; P:cell proliferation; ISS.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR007701; IFRD.
DR InterPro; IPR006921; IFRD_C.
DR Pfam; PF05004; IFRD; 1.

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DR Pfam; PF04836; IFRD C; 1.
SQ SEQUENCE 442 AA; 48047 MW; CB54F2118C0CBA74 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 140 GALESLR 146
|||||
DB 94 GALESLR 100
RESULT 33
ID ICE8 MOUSE STANDARD; PRT; 480 AA.
AC O8910; O35669;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-8 precursor (EC 3.4.22.-).
GN CASP8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=129/SVJ;
RX MEDLINE=98318661; PubMed=9654089;
RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
RT "Molecular cloning and characterization of mouse caspase-8";
RL Eur. J. Biochem. 253:399-405(1998).
[2]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99057979; PubMed=9837723;
RA Van de Craen M., Van Loo G., Declercq W., Schotte P.,
RA van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
RT Vandenabeele P.;
RT "Molecular cloning and identification of murine caspase-8";
RL J. Mol. Biol. 284:1017-1026(1998).
[3]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
SEQUENCE OF 57-476 FROM N.A.
RA Kioschis P., Kischkel F., Poustka A., Kramer P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic

activation. The active dimeric enzyme is then liberated from the DISC and free to activate downstream apoptotic proteases. Proteolytic fragments of the N-terminal propeptide (termed CAP3, CAP5 and CAP6) are likely retained in the DISC. Cleaves and activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May participate in the G2M6 apoptotic pathways. Cleaves ADPRT. Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC. Likely target for the coxop virus CRMA death inhibitory protein. -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35. -!- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit. Interacts with Fadd, Cflar and Peals (By similarity). -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues. Highest expression in spleen, thymus, lung, liver and kidney. Lower expression in heart, brain, testis and skeletal muscle. -!- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at day 7. -!- PTM: Generation of the subunits requires association with the death-inducing signaling complex (DISC), whereas additional processing is likely due to the autocatalytic activity of the activated protease. G2MB and CASP10 can be involved in these processing events (By similarity). -!- SIMILARITY: Belongs to peptidase family C14. -!- SIMILARITY: Contains 2 death effector (DED) domains.

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EMBL; AF067841; AAC40132.1; -
EMBL; AF067835; AAC40132.1; JOINED.
EMBL; AF067836; AAC40132.1; JOINED.
EMBL; AF067837; AAC40132.1; JOINED.
EMBL; AF067838; AAC40132.1; JOINED.
EMBL; AF067839; AAC40132.1; JOINED.
EMBL; AF067840; AAC40132.1; JOINED.
EMBL; AF067834; AAC40131.1; -
EMBL; AJ007749; CAA07677.1; -
EMBL; BC006737; AAH06737.1; -
EMBL; BC049955; AAH49955.1; -
EMBL; AJ000641; CAA04196.1; -
HSSP; Q15806; 1QDU.
MEROPS; C14.009; -
MGD; MGI:1261423; Casp8.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0004205; F:caspase-8 activity; IDA.
GO; GO:0006915; P:apoptosis; IDA.
InterPro; IPR001875; DED.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF01335; DED; 2.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
SMART; SM00031; DED; 2.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS02007; CASPASE_P10; 1.
PROSITE; PS02008; CASPASE_P20; 1.
PROSITE; PS0168; DED; 2.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat.
FT PROPEP 1 218 BY SIMILARITY.
FT CHAIN 219 376 CASPASE-8 SUBUNIT P18.
FT PROPEP 377 387 BY SIMILARITY.
FT CHAIN 388 480 CASPASE-8 SUBUNIT P10.
FT ACT_SITE 319 319 BY SIMILARITY.
FT ACT_SITE 362 362 BY SIMILARITY.
FT DOMAIN 3 80 DED 1.

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EMBL; M24424; AAA27189.1; -
 EMBL; AJ272210; CAB75592.1; -
 EMBL; AE008753; AAL20159.1; -
 STyGene; SG10294; phoQ.
 InterPro; IPR003594; ATPbind_ATPase.
 InterPro; IPR004358; Bact_sens_pr_C.
 InterPro; IPR003660; HAMP.
 InterPro; IPR003661; His_kinA_N.
 InterPro; IPR005467; His_kinase.
 Pfam; PF00672; HAMP; 1.
 Pfam; PF02518; HATPase_c; 1.
 Pfam; PF00512; Hiska; 1.
 PRINTS; PR00344; BCTRLSENSOR.
 SMART; SM00387; HATPase_c; 1.
 SMART; SM00388; Hiska; 1.
 PROSITE; PS50109; HIS_KIN; 1.
 Sensory transduction; Transferase; Kinase; Phosphorylation;
 Transmembrane; Inner membrane; Growth regulation; Virulence;
 Complete proteome.
 DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 17 37 POTENTIAL.
 DOMAIN 38 194 PERIPLASMIC (POTENTIAL).
 TRANSMEM 195 215 POTENTIAL.
 DOMAIN 216 487 CYTOPLASMIC (POTENTIAL).
 DOMAIN 216 266 HAMP.
 DOMAIN 274 481 HISTIDINE KINASE.
 MOD_RES 277 277 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 VARIANT 82 99 MISSING (IN STRAIN ATCC 10428).
 VARIANT 442 459 MISSING (IN STRAIN ATCC 10428).
 MUTAGEN 313 313 R->W: INCREASED ABILITY TO PROLIFERATE WITHIN FIBROBLASTS.
 SEQUENCE 487 AA; 55466 MW; BDCFEFC56F4CA058 CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 487;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 VLLSREL 34
 |||||
 Db 332 VLLSREL 338

RESULT 35
 VRK2 MOUSE STANDARD; PRT; 503 AA.
 AC Q8BNZ1; Q8BPU8; Q8CJ46; Q91WS1; Q9CZF9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine protein kinase VRK2 (EC 2.7.1.37) (Vaccinia-related kinase 2).
 DE Kinase 2).
 GN VRK2
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6;
 RX PubMed=12417526;
 RA Agoulis A.I., Lu B., Zhu Q., Truong C., Ty M.T., Arango N., Chada K.K., Bishop C.E.;
 RA "A novel gene, Pog, is necessary for primordial germ cell proliferation in the mouse and underlies the germ cell deficient mutation, gcd.";
 RL Hum. Mol. Genet. 11:3047-3053(2002).
 RN [2]

FT DOMAIN 101 177 DED 2.
 FT CONFLICT 68 71 HISR -> PHPVG (IN REF. 4).
 FT CONFLICT 94 99 DNAQIS -> RQCRFL (IN REF. 4).
 FT CONFLICT 96 96 A -> V (IN REF. 2).
 FT CONFLICT 103 107 VMLFK -> SCSEF (IN REF. 4).
 FT CONFLICT 475 475 K -> N (IN REF. 4).
 SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5ED4F CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 480;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 LRKKLFF 413
 |||||
 Db 472 LRKKLFF 478

RESULT 34
 PHOQ_SALTY STANDARD; PRT; 487 AA.
 ID PHOQ_SALTY STANDARD; PRT; 487 AA.
 AC P14147; Q9L3L1;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Virulence sensor protein phoQ (EC 2.7.3.-).
 GN PHOQ OR STM1230.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14028;
 RX MEDLINE=89296942; PubMed=2544889;
 RA Miller S.I., Kukral A.M., Mekalanos J.J.;
 RA "A two-component regulatory system (phoP phoQ) controls Salmonella typhimurium virulence.";
 RT typhimurium virulence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5054-5058(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-313.
 RC STRAIN=SL1344;
 RX MEDLINE=21437654; PubMed=11553591;
 RA Cano D.A., Martinez-Moya M., Pucciarelli M.G., Groisman E.A., Casadesus J., Garcia-del Portillo F.;
 RA "Salmonella enterica serovar typhimurium response involved in attenuation of pathogen intracellular proliferation.";
 RL Infect. Immun. 69:6463-6474(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
 RA "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: Member of the two-component regulatory system phoQ/phoP which regulates the expression of genes involved in virulence and promotes intramacrophage survival of S.typhimurium. Is required to attenuate bacterial growth within fibroblast cells. PhoQ may function as a membrane-associated protein kinase that phosphorylates phoP in response to environmental signals.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (probable).
 CC -!- SIMILARITY: Contains 1 HAMP domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
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SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4).
 RP STRAIN=C57BL/6J; TISSUE=Embryo, Eye, and Spleen;
 RX MEDLINE=22354683; PubMed=1246881;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Iagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guttingich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kanyaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yangigisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Nakamura K., Sakazume N., Sato K.,
 RA Hironaka-Kishikawa T., Konno H., Nakamura K., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RN TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [4]
 RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX MEDLINE=22666352; PubMed=12782311;
 RA Vega F.M., Gonzalo P., Gaspar M.L., Lazo P.A.;
 RT "Expression of the VRK (vaccinia-related kinase) gene family of p53
 RT regulators in murine hematopoietic development";
 RL FEBS Lett. 544:176-180 (2003).
 CC -!- FUNCTION: Probable serine/threonine kinase (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=QB2N21-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=QB2N21-2; Sequence=VSP_008543;
 CC Note=No experimental confirmation available;
 CC PRT; 504 AA.

CC Name=3;
 CC IsoId=QB2N21-3; Sequence=VSP_008541, VSP_008542;
 CC Note=No experimental confirmation available;
 CC Name=4;
 CC IsoId=QB2N21-4; Sequence=VSP_008539, VSP_008540;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Expressed in liver, kidney and muscle. Weakly
 CC expressed in thymus, bone marrow and spleen.
 CC -!- DEVELOPMENTAL STAGE: Weakly expressed in embryo compared to VRK1
 CC and VRK3. Expressed from E10.5 to E14 in developing liver and then
 CC decreases. It increases again from E17.5 and remains thereafter.
 CC Highly expressed in hematopoietic embryonic tissues from E10.5 to
 CC E14.5. Weakly expressed in the yolk-sac.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. VRK
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL; AF513620; AAN64922.1; -;
 CC EMBL; AK012664; BAB28393.1; -;
 CC EMBL; AK053297; BAC35335.1; -;
 CC EMBL; AK089825; BAC40370.1; -;
 CC EMBL; BC013520; AAH13520.1; -;
 CC HSSP; Q06486; 1CKI.
 CC MGD; MGI:1917172; Vrk2.
 CC InterPro; IPR000719; Prot kinase.
 CC ProDom; PD000001; Prot kinase, 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
 CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Transmembrane; Alternative splicing.
 CC TRANSMEM 482 502 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
 CC (POTENTIAL).
 CC DOMAIN 29 313 PROTEIN KINASE (BY SIMILARITY).
 CC NP_BIND 35 61 ATP (BY SIMILARITY).
 CC FT ACT_SITE 166 166 BY SIMILARITY.
 CC FT VARSPPLIC 115 115 S -> R (in isoform 4).
 CC FT VARSPPLIC 116 503 /FTId=VSP_008539.
 CC FT VARSPPLIC 151 163 Missing (in isoform 4).
 CC FT VARSPPLIC 151 163 /FTId=VSP_008540.
 CC FT VARSPPLIC 151 163 LDVLEYIHENEYV -> VSLRLDTGDLDDI (in
 CC isoform 3).
 CC FT VARSPPLIC 164 503 /FTId=VSP_008541.
 CC FT VARSPPLIC 342 390 Missing (in isoform 3).
 CC FT VARSPPLIC 342 390 /FTId=VSP_008542.
 CC FT CONFLICT 33 33 Missing (in isoform 2).
 CC FT CONFLICT 226 226 K -> R (IN REF. 1).
 CC FT CONFLICT 319 319 A -> P (IN REF. 2).
 CC FT CONFLICT 333 333 P -> L (IN REF. 3).
 CC FT CONFLICT 333 333 H -> R (IN REF. 3).
 CC SQ SEQUENCE 503 AA; 58118 MW; 6F29E3E412ECB221 CRC64;
 CC Query Match 1.7%; Score 7; DB 1; Length 503;
 CC Best Local Similarity 100.0%; Pred. No. 77;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 131 IGSQGF 137
 CC DB 35 IGSQGF 41
 CC RESULT 36
 CC PSD5_HUMAN
 CC ID Q8B2N21-2; Sequence=VSP_008543;
 CC AC Q16401; Q15045; STANDARD; PRT; 504 AA.

DR EMBL; BC014478; AAI14478.1; -.
 DR EMBL; D31889; BAA06897.1; -.
 DR Genew; HGNC:9563; PSMD5.
 DR GK; Q16401; -.
 DR MM; 604452; -.
 DR GO; GO:0005837; C:26S proteasome; TAS.
 DR InterPro; IPR008938; ARM.
 KW Proteasome.
 SQ SEQUENCE 504 AA; 56195 MW; 30F31602DDF4EF89 CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 504;
 Best Local Similarity 100.0%; Pred. No. 77; 0; Indels 0;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;
 Qy 329 LDAISSL 335
 Db 362 LDAISSL 368
 RESULT 37
 SPKD SYNY3 STANDARD; PRT; 505 AA.
 AC P54735;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Serine/threonine-protein kinase D (EC 2.7.1.37).
 GN SPKD OR SL0776.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 ON NCBI_TaxID=1148;
 RX MEDLINE=22159630; PubMed=12169951;
 RA Kamei A., Yusa T., Geng X., Ikeuchi M.;
 RT "Biochemical examination of the potential eukaryotic-type protein
 RT kinase genes in the complete genome of the unicellular Cyanobacterium
 RT Synechocystis sp. PCC 6803.";
 RL DNA Res. 9:71-78 (2002).
 RN [2]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166 (1995).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC
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 CC
 CC EMBL; AB046600; BAB17036.1; -.
 DR EMBL; D64005; BAA10726.1; -.
 DR PIR; S77034; S77034.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR003646; SH3_bac.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00287; SH3b; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Complete proteome.

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 26S proteasome non-ATPase regulatory subunit 5 (26S proteasome
 DE subunit S5B) (26S protease subunit S5 basic).
 GN PSMD5 OR KIAA0072.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 75-96; 311-337 AND 431-449.
 RC TISSUE=Breast cancer;
 RX MEDLINE=96007524; PubMed=7559544;
 RA Devereux Q., Jensen C., Rechsteiner M.;
 RT "Molecular cloning and expression of a 26 S protease subunit enriched
 RT in dileucine repeats.";
 RL J. Biol. Chem. 270:23726-23729 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE OF 2-504 FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=96051398; PubMed=7584044;
 RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
 RA Seki N., Kawabayashi Y., Ishikawa K.-I., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. II.
 RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
 RT analysis of cDNA clones from human cell line KG-1.";
 RL DNA Res. 1:223-229 (1994).
 CC -!- FUNCTION: Belongs to the 26S multisubunit protease, which is
 CC required for ubiquitin-dependent proteolysis. Does not bind
 CC ubiquitin polymers.
 CC -!- SUBUNIT: 26S protease is composed of a multicatalytic protease
 CC (proteasome) and a regulatory ATPase complex. Both are
 CC multisubunit structures that associate in the presence of ATP to
 CC form the protease. Subunit S5B is part of the regulatory complex.
 CC -!- DOMAIN: Rich in dileucine repeats, which have been implicated in
 CC trafficking of a variety of transmembrane proteins.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S5B FAMILY.
 CC
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 CC EMBL; S79862; AAB35397.1; -.
 KW

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FT DOMAIN          9 271 PROTEIN KINASE.
FT NP BIND         15 23  ATP (BY SIMILARITY).
FT BINDING         40 40  ATP (BY SIMILARITY).
FT ACT SITE       136 136  BY SIMILARITY.
SQ SEQUENCE       505 AA: 55213 MW;  C4F12A186C4D51C CRC64;

Query Match      1.7%; Score 7; DB 1; Length 505;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGD 138
Db 16 GSGGFGD 22

RESULT 38
VRK2 HUMAN
ID VRK2_HUMAN STANDARD; PRT; 508 AA.
AC Q86Y07; Q86Y09; Q86Y10; Q86Y11; Q86Y12; Q86Y15; Q99987;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase VRK2 (EC 2.7.1.37) (Vaccinia-related
DE kinase 2).
GN VRK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=98008921; PubMed=9344656;
RA Nezu J.-I., Oku A., Jones M.H., Shimane M.;
RT "Identification of two novel human putative serine/threonine kinases,
RT VRK1 and VRK2, with structural similarity to Vaccinia virus B1R
RT Kinase.";
RL Genomics 45:327-331(1997).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 2).
RA Blanco S., Klimcakova L., Santos C., Sevilla A., Lazo P.A.;
RT "Expression of a variant isoform of the human vaccinia-related kinase
RT 2 (VRK2B) and its effects on p53 dependent transcription.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5), AND VARIANT ILE-167.
RA Suriyaputra S.P., Sarfarazi M.;
RT "Identification of 6 different isoforms for Vaccinia-related kinase 2
RT (VRK2) gene.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buertow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heitton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Probable serine/threonine kinase (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=1;
CC IsoId=Q86Y07-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q86Y07-2; Sequence=VSP_008537, VSP_008538;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q86Y07-3; Sequence=VSP_008533;
CC Note=No experimental confirmation available;
CC Name=4; Synonyms=5;
CC IsoId=Q86Y07-4; Sequence=VSP_008534;
CC Note=No experimental confirmation available;
CC Name=5; Synonyms=6;
CC IsoId=Q86Y07-5; Sequence=VSP_008535, VSP_008536;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in fetal
CC liver, skeletal muscle, pancreas, heart, peripheral blood
CC leukocytes and testis.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. VRK
CC subfamily.
CC
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CC EMBL: AB000450; BAA19109.1; -
CC EMBL: AJ512204; CAD54446.2; -
CC EMBL: AY228367; AAO73047.1; -
CC EMBL: AY228368; AAO73048.1; -
CC EMBL: AY228369; AAO73049.1; -
CC EMBL: AY228370; AAO73050.1; -
CC EMBL: AY228371; AAO73051.1; -
CC EMBL: AY228372; AAO73052.1; -
CC EMBL: BC027854; AAH27854.1; -
CC HSP; Q06486; LCKI.
CC Genew; HGNC:12719; VRK2.
CC MIM: 602169; -
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR008271; Ser_thr_pkin_AS.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc_1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Transmembrane; Serine/threonine-protein kinase; ATP-binding;
CC Transmembrane; Alternative splicing; Polymorphism.
CC TRANSMEM 487 507 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
CC (POTENTIAL).
CC DOMAIN 29 319 PROTEIN KINASE.
CC NP_BIND 35 61 ATP (BY SIMILARITY).
CC ACT_SITE 166 166 BY SIMILARITY.
CC VARSPLIC 1 23 Missing (in isoform 3).
CC VARSPLIC 1 118 /FTId=VSP_008533.
CC VARSPLIC 395 396 Missing (in isoform 4).
CC VARSPLIC 397 508 ES -> PR (in isoform 5).
CC VARSPLIC 395 400 /FTId=VSP_008536.
CC VARSPLIC 401 508 ESTRRR -> GRSIGY (in isoform 2).
CC VARSPLIC 401 508 Missing (in isoform 2).

```

Tue Aug 3 09:36:14 2004

us-09-961-201a-1.oligo.rsp

FT VARIANT 167 167 /FTID=VSP_008538.
 FT FTID=VAR_017095.
 FT CONFLICT 419 419 K -> E (IN REF. 3;
 FT AAO73048/AAO73049/AAO73051).
 SQ SEQUENCE 508 AA; 58126 MW; 157FBF8F48511AF4 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 508;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 131 IGSFGFG 137
 Db 35 IGSFGFG 41

RESULT 39
 SYK_HALN1 STANDARD; PRT; 548 AA.

AC Q9HNN7; (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
 GN LYSS OR VNG2017G.
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2504483; PubMed=11016950;
 RA NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Laskey S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B.G., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,
 RA "Genome sequence of Halobacterium species NRC-1."
 RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
 CC + L-lysyl-tRNA(Lys).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.

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 CC -----
 CC EMBL; AE005095; AAG20183.1; -.
 CC F01; C84352; C84352.
 CC HAMAP; MF_00177; -; 1.
 CC InterPro; IPR002904; Lys tRNA-synt 1c.
 CC InterPro; IPR008925; tRNA-synt bind.
 CC InterPro; IPR001412; tRNA-synt 1.
 CC Pfam; PF01921; tRNA-synt 1f; 1.
 CC TIGRfam; TIGR00467; lysE_arch; 1.
 CC PROSITE; PS00178; AA tRNA LIGASE I; 1.
 CC KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 CC Complete proteome.

FT SITE 43 51 "HIGH" REGION.
 FT SITE 308 312 "KWSK" REGION.
 SQ SEQUENCE 548 AA; 60874 MW; 85DC68AC77FD48 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 548;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 VLALLEL 219
 Db 322 VLALLEL 328

RESULT 40

E2K2 HUMAN STANDARD; PRT; 551 AA.
 ID E2K2_HUMAN
 AC P19525;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interferon-induced, double-stranded RNA-activated protein kinase
 DE (EC 2.7.1.-) (Interferon-inducible RNA-dependent protein kinase) (p68
 DE kinase) (p1/eIF-2A protein kinase).
 GN PKR OR EIF2AK2 OR PKR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 101-118 AND 309-325.
 RX MEDLINE=90322433; PubMed=1695551;
 RA Meurs E., Chong K., Galabru J., Thomas N.S.B., Kerr I.M.,
 RA Williams B.R.G., Hovanessian A.G.;
 RA "Molecular cloning and characterization of the human double-stranded
 RT RNA-activated protein kinase induced by interferon."
 RL Cell 62:379-390(1990).
 RN [2]

RP REVISIONS.
 RP Meurs E.;
 RL Submitted (XXX-1990) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92230231; PubMed=1373553;
 RA Thomas D.C., Doonan J.P., Samuel C.E.;
 RA "Mechanism of interferon action: cDNA structure, expression, and
 RT regulation of the interferon-induced, RNA-dependent p1/eIF-2 alpha
 RT protein kinase from human cells."
 RL Virology 188:33-46(1992).
 RN [4]

RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96411668; PubMed=8812437;
 RA Kuhen K.L., Shen X., Carlisle E.R., Richardson A.L., Weier H.U.G.,
 RA Tanaka H., Samuel C.E.;
 RA "Structural organization of the human gene (PKR) encoding an
 RT interferon-inducible RNA-dependent protein kinase (PKR) and
 RL differences from its mouse homolog."
 RL Genomics 36:197-201(1996).
 RN [5]

RP SEQUENCE FROM N.A.
 RP Bieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP MUTAGENESIS, AND AUTOPHOSPHORYLATION OF THR-446 AND THR-451.
 RX MEDLINE=211326157; PubMed=11337501;
 RA Zhang F., Romano P.R., Nagamura-Inoue T., Tian B., Dever T.E.,
 RA Mathews M.B., Ozato K., Hinnebusch A.G.;
 RA "Binding of double-stranded RNA to protein kinase PKR is required for
 RT dimerization and promotes critical autophosphorylation events in the
 RT activation loop."
 RL J. Biol. Chem. 276:24946-24958(2001).
 RN [7]

RP STRUCTURE BY NMR OF 1-175.
 RX MEDLINE=98409549; PubMed=9736623;
 RA Nanduri S., Carpick B.W., Yang Y., Williams B.R., Qin J.;
 RA "Structure of the double-stranded RNA-binding domain of the protein
 RT kinase PKR reveals the molecular basis of its dsRNA-mediated
 RT activation."
 RN [8]

```

EMBO J. 17:5458-5465(1998).
-!- FUNCTION: On activation by double-stranded RNA in the presence of
ATP, the kinase becomes autophosphorylated and can catalyze the
phosphorylation of the alpha subunit of EIF2, which leads to an
inhibition of the initiation of protein synthesis.
-!- ENZYME REGULATION: Activity is markedly stimulated by manganese
ions. Besides dsRNA, heparin is a potent activator of the kinase.
Binding to dsRNA is required for dimerization leading to
autophosphorylation in the activation loop and stimulation of
function.
-!- SUBUNIT: Homodimer.
-!- INDUCTION: By interferon.
-!- PTM: Autophosphorylated on several Ser and Thr residues.
Autophosphorylation of Thr-451 is dependent on Thr-446 and is
stimulated by dsRNA binding and dimerization.
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. GCN2
subfamily.
-!- SIMILARITY: Contains 2 DRBM (double-stranded RNA-binding) domains.
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DR EMBL; M35663; AAA36409.1; -
DR EMBL; M85294; AAA18253.1; -
DR EMBL; U50648; AAC50768.1; -
DR EMBL; U50634; AAC50768.1; JOINED.
DR EMBL; U50635; AAC50768.1; JOINED.
DR EMBL; U50636; AAC50768.1; JOINED.
DR EMBL; U50637; AAC50768.1; JOINED.
DR EMBL; U50638; AAC50768.1; JOINED.
DR EMBL; U50639; AAC50768.1; JOINED.
DR EMBL; U50640; AAC50768.1; JOINED.
DR EMBL; U50641; AAC50768.1; JOINED.
DR EMBL; U50642; AAC50768.1; JOINED.
DR EMBL; U50643; AAC50768.1; JOINED.
DR EMBL; U50644; AAC50768.1; JOINED.
DR EMBL; U50645; AAC50768.1; JOINED.
DR EMBL; U50646; AAC50768.1; JOINED.
DR EMBL; U50647; AAC50768.1; JOINED.
DR EMBL; AY228338; AAC38055.1; -
DR PIR; JC5225; JC5225.
DR FDB; LQ6; 23-DEC-99.
DR Genew; HGNC:9437; PRKR.
DR MIM; 176871; -
DR GO; GO:0003725; F:double-stranded RNA binding; TAS.
DR GO; GO:0004694; F:eukaryotic translation initiation factor 2a. . ; TAS.
DR GO; GO:0008601; F:protein phosphatase type 2A, intrinsic regu. . ; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00035; dsrm; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00358; DS_RBD; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_SF; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Phosphorylation; Interferon induction; RNA-binding; 3D-structure.
FT DOMAIN 59 75 DRBM 1.
FT DOMAIN 149 165 DRBM 2.
FT DOMAIN 267 538 PROTEIN KINASE.
FT NP_BIND 273 281 ATP (BY SIMILARITY).
EMBO J. 17:5458-5465(1998).
ATP.
BY SIMILARITY.
2 X 13 AA APPROXIMATE REPEATS.
1.
2.
PHOSPHORYLATION (AUTO-).
PHOSPHORYLATION (AUTO-).
SK-AA: IN FL-PKR-2A1; MODERATE LOSS OF
ACTIVITY BUT NO EFFECT ON DSRNA BINDING.
K-AA: IMPAIRS DSRNA BINDING BUT NOT
DIMERIZATION OR ACTIVITY.
A-SE: SIGNIFICANT LOSS OF ACTIVITY; LOSS
OF DSRNA BINDING AND DIMERIZATION.
TK-AA: IN FL-PKR-2A1I; NO EFFECT ON
ACTIVITY.
MISSING: LOSS OF ACTIVITY.
T-AA: MODERATE LOSS OF ACTIVITY.
K-AR: LOSS OF ACTIVITY.
T-AA: SIGNIFICANT LOSS OF ACTIVITY AND
IMPACTS AUTOPHOSPHORYLATION OF THR-451.
T-AA: LOSS OF ACTIVITY.
T-AA: LOSS OF ACTIVITY.
815AD83ACAB45DA3 CRC64;
62094 MW;
Score 7; DB 1; Length 551;
Query Match 1.7%;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 IGSGGFG 137
Db 273 IGSGGFG 279
|||||
|||||
RESULT 41
GGT_PSESP STANDARD; PRT; 575 AA.
AC P36267;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2).
GN GGT.
OS Pseudomonas sp. (strain Al4).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93305254; PubMed=7765305;
RA Ishiye M., Yamashita M., Niwa M.;
RT "Molecular cloning of the gamma-glutamyltranspeptidase gene from a
Pseudomonas strain."
RL Biotechnol. Prog. 9:323-331(1993).
CC -!- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid =
peptide + 5-L-glutamyl-amino acid.
CC -!- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A
PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.
CC -!- SUBUNIT: This enzyme consists of two polypeptide chains, which are
synthesized in precursor form from a single polypeptide.
CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the gamma-glutamyltransferase family.
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DR EMBL; S63255; AAC60442.1; -
DR MEROPS; T03.001; -
DR InterPro; IPR000101; Peptidase_T3.
DR Pfam; PF01019; G-glu transpept; 1.
DR PRINTS; PR01210; GGTRANSPTASE.

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DR TIGRFAMS: TIGR00066; g glut trans; 1.
 DR PROSITE; PS00462; G_GLU_TRANSPHEPTIDASE; 1.
 KW Transferase; Acyltransferase; Periplasmic; Zymogen; Signal;
 KW Glutathione biosynthesis.
 FT SIGNAL 1 24
 FT CHAIN 25 376 GAMMA-GLUTAMYLTRANSFERASE LARGE CHAIN.
 FT CHAIN 377 575 GAMMA-GLUTAMYLTRANSFERASE SMALL CHAIN.
 FT BINDING 450 450 GAMMA-GLUTAMYL (POTENTIAL).
 FT SEQUENCE 575 AA; 61301 MW; CF2EB69F02CD0201 CRC64;
 SQ
 Query Match 1.7%; Score 7; DB 1; Length 575;
 Best Local Similarity 100.0%; Pred.No. 87;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 273 PSLGGKP 279
 DB 547 PSLGGKP 553
 RESULT 42
 LU_HUMAN
 ID LU_HUMAN STANDARD; PRT; 628 AA.
 AC P50895;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lutheran blood group glycoprotein precursor (B-CAM cell surface
 DE glycoprotein) (Aubergier B antigen) (F8/G253 antigen).
 GN LU OR BCAM OR MGK19.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-67 AND 182-203.
 RX MEDLINE=95296337; PubMed=7777537;
 RA Parsons S.F., Mallinson G., Holmes C.H., Houlihan J.M., Simpson K.L.,
 RA Mawby W.J., Spurr N.K., Warne D., Barclay A.N., Anstee D.J.;
 RT "The Lutheran blood group glycoprotein, another member of the
 RT immunoglobulin superfamily, is widely expressed in human tissues and
 RT is developmentally regulated in human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5496-5500(1995).
 RN [2]
 RP SEQUENCE OF 1-588 FROM N.A.
 RX MEDLINE=95042297; PubMed=7954395;
 RA Campbell I.G., Foulkes W.D., Senger G., Trowsdale J.,
 RA Garin-Chesa P., Rettig W.J.;
 RT "Molecular cloning of the B-CAM cell surface glycoprotein of
 RT epithelial cancers: a novel member of the immunoglobulin
 RT superfamily.";
 RL Cancer Res. 54:5761-5765 (1994).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITE ASN-439.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H., Li X.-J., Martin D.B., Aebbersold R.;
 RT "Identification and quantification of N-linked glycoproteins using
 RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
 RL Nat. Biotechnol. 21:660-666(2003).
 CC -!- FUNCTION: PROBABLE RECEPTOR. MAY MEDIATE INTRACELLULAR SIGNALING.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION (HIGHEST IN THE
 CC PANCREAS AND VERY LOW IN BRAIN). CLOSELY ASSOCIATED WITH THE BASAL
 CC LAYER OF CELLS IN EPITHELIA AND THE ENDOTHELIUM OF BLOOD VESSEL
 CC WALLS.
 CC -!- DEVELOPMENTAL STAGE: Is under developmental control in liver and
 CC may also be regulated during differentiation in other tissues.
 CC Upregulated following malignant transformation in some cell types.
 CC -!- POLYMORPHISM: LU is responsible for the Lutheran blood group
 CC system.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -!- DATABASE: NAMB=Blood group antigen mutation database;

NOTE=Lutheran (Lu) blood group system;
 WWW="http://www.bioc.aecom.yu.edu/bgmut/lutheran.htm".
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 EMBL; X83425; CAA58449.1; -;
 EMBL; X80026; CAA56327.1; -;
 PIR; I37202; I37202.
 PIR; I38000; I38000.
 Genew; HGNC:6722; LU.
 MIM; 111200; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS50835; IG_LIKE; 5.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
 KW Repeat; Blood group antigen.
 FT SIGNAL 1 31
 FT CHAIN 32 628 LUTHERAN BLOOD GROUP GLYCOPROTEIN.
 FT DOMAIN 32 547 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 548 568 POTENTIAL.
 FT DOMAIN 569 628 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 142 IG-LIKE V-TYPE 1.
 FT DOMAIN 147 257 IG-LIKE V-TYPE 2.
 FT DOMAIN 274 355 IG-LIKE C2-TYPE 1.
 FT DOMAIN 363 441 IG-LIKE C2-TYPE 2.
 FT DOMAIN 448 541 IG-LIKE C2-TYPE 3.
 FT DISULFID 53 125 PROBABLE.
 FT DISULFID 172 237 PROBABLE.
 FT DISULFID 291 337 PROBABLE.
 FT DISULFID 384 424 PROBABLE.
 FT DISULFID 473 522 PROBABLE.
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 377 377 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 225 226 RL -> PC (IN REF. 2).
 FT CONFLICT 355 356 EL -> DV (IN REF. 2).
 SQ SEQUENCE 628 AA; 67374 MW; C89B0A4835492B1E CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 628;
 Best Local Similarity 100.0%; Pred.No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 132 GSGGFGD 138
 DB 620 GSGGFGD 626
 RESULT 43
 UL47_HSV1F
 ID UL47_HSV1F STANDARD; PRT; 664 AA.
 AC P08313;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Virion protein UL47 (82/81 kDa tegument protein) (VMW82/81) (VP13/14).
 GN UL47.
 OS Herpes simplex virus (type 1 / strain F).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.

DR InterPro; IPR002937; Amino_oxidase.
DR InterPro; IPR006064; Glycosidase.
DR InterPro; IPR000205; NAD BS.
DR Pfam; PF01593; Amino_oxidase; 1.
DR Pfam; PF02027; RoLB RoLC; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR OXIDOREDUCTASE; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
KW Plasmid.
SQ SEQUENCE 755 AA; 83972 MW; 6FA63E502343136F CRC64;

Query Match 1.7%; Score 7; DB 1; Length 755;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSGGFG 137
|||||||
DB 436 IGSGGFG 442

RESULT 47
YQ34 MYCTU STANDARD; PRT; 778 AA.
ID YQ34 MYCTU
AC P71933;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical PE-PGRS family protein RV2634C/MT2712/MB2667C.
GN RV2634C OR MT2712 OR MTCY441.04C OR MB2667C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
[1]
SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
[2]
SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RA MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland R., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J.C., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).
[3]
SEQUENCE FROM N.A.
SPECIES=M.bovis; STRAIN=AF2122/97;
RA MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsenpe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RA "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003)
CC -!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
CC SUBFAMILY.
CC -----

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DR EMBL; Z80225; CAB02341.1; -.
 DR EMBL; AE007103; AAK47026.1; ALT_INIT.
 DR EMBL; BX248343; CAD94852.1; -.
 DR PIR; F70963; F70963.
 DR TIGR; MT2712; -.
 DR TubercuList; Rv2634c; -.
 DR InterPro; IPR000084; PE_region.
 DR Pfam; PF00934; PE; 1.
 DR ProDom; PD001223; PE_region; 1.
 DR KW Hypothetical protein; Complete proteome.
 FT CONFLICT 51 51 V -> L (IN REF. 2).
 FT CONFLICT 63 63 Q -> H (IN REF. 2).
 FT CONFLICT 274 274 A -> T (IN REF. 2).
 SQ SEQUENCE 778 AA; 63131 MW; DAB20FE5BE4999E7 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 778;
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSGGFG 137
 DB 223 IGSGGFG 229

RESULT 48

HIFA_XENLA
 ID HIFA_XENLA STANDARD; PRT; 805 AA.
 AC Q918A9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
 GN HIFA.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kietzmann T.;
 RT "Cloning and expression of the Xenopus laevis hypoxia inducible factor
 1 alpha homologue";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Functions as a master transcriptional regulator of the
 CC adaptive response to hypoxia. Binds to core DNA sequence 5'-
 CC [AG]CGTG-3' within the hypoxia response element (HRE) of target
 CC gene promoters. Activation requires recruitment of transcriptional
 CC coactivators (By similarity).
 CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
 CC alpha and a beta/ARNT subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
 CC translocation in response to hypoxia (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC
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DR EMBL; AJ277829; CAB96628.1; -.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR001321; Hypoxindf1A.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS_domain.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 2.
 DR PRINTS; PR01080; HYPOXIAIFA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50888; HLH; FALSE_NEG.
 DR PROSITE; PS50112; PAS; 2.
 DR Transcription regulation; Activator; Nuclear protein; DNA-binding;
 KW Repeat.
 KW DNA_BIND 17 30 BASIC DOMAIN.
 FT DOMAIN 31 71 HELIX-LOOP-HELIX MOTIF.
 FT DOMAIN 85 157 PAS 1.
 FT DOMAIN 229 300 PAS 2.
 FT DOMAIN 303 346 PAC.
 SQ SEQUENCE 805 AA; 90964 MW; BABFA0BD6B44FF3B CRC64;

Query Match 1.7%; Score 7; DB 1; Length 805;
 Best Local Similarity 100.0%; Pred.No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 LRTFDQL 329
 DB 570 LRTFDQL 576

RESULT 49

CAPP_SYNEL
 ID CAPP_SYNEL STANDARD; PRT; 1011 AA.
 AC Q34QB2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
 GN PPC OR SVPEPC OR PLL1912.
 OS Synechococcus elongatus (Thermosynechococcus elongatus), and
 OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=32046; 32053;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.elongatus; STRAIN=BP-1;
 RX MEDLINE=2225144; PubMed=12240834;
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
 RA Watanabe A., Iriiguchi M., Kawashima K., Kimura T., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Makazaki N.,
 RA Shimpou S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the thermophilic cyanobacterium
 Thermosynechococcus elongatus BP-1";
 RL DNA Res. 9:123-130(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.vulcanus;
 RX Chen L.M., Omiya T., Hata S., Inoue Y., Izui K.;
 RT "Molecular characterization of Synechococcus vulcanus
 phosphoenolpyruvate carboxylase";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
 CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
 CC the tricarboxylic acid cycle.
 CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
 CC phosphoenolpyruvate + CO(2).
 CC -!- PATHWAY: Tricarboxylic acid cycle.
 CC -!- SIMILARITY: Belongs to the PEPCase family.
 CC
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us-09-961-201a-1.oligo.rsp

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CC -----

DR EMBL; AP005375; BAC09464.1; -;
DR EMBL; AB057454; BAB64533.1; -;
DR HAMAP; MF 00595; -; 1.
DR InterPro; IPR001449; PEPcase.
DR Pfam; PF00311; PEPcase; 1.
DR PRINTS; PR00150; PEPcase; 1.
DR PROSITE; PS00781; PEPcase_1; FALSE_NEG.
DR PROSITE; PS00393; PEPcase_2; 1.
KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
KW Complete proteome.
FT ACT_SITE 207 BY SIMILARITY.
FT ACT_SITE 658 BY SIMILARITY.
FT ACT_SITE 658 BY SIMILARITY.
SQ SEQUENCE 1011 AA; 116426 MW; 0A11D4D01FE9E7FE CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RLRLVEE 19
Db 27 RLRLVEE 33

RESULT 50

UL70_HCMVA STANDARD; PRT; 1062 AA.
ID UL70_HCMVA STANDARD; PRT; 1062 AA.
AC P17149;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Helicase/primase complex protein (Probable DNA replication protein
DE UL70).
GN UL70.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horneill T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RA "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169".
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -!- FUNCTION: Involved in DNA replication.
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52,
CC EBV-1 7, EBV BSLF1, HVS-1 56, HCMV UL70 AND VZV 6.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17403; CA335386.1; -;
DR PIR; S09834.
DR InterPro; IPR004340; UL52 UL70.
DR Pfam; PF03121; UL52 UL70; 1.
KW DNA replication.
SQ SEQUENCE 1062 AA; 120925 MW; F3B8DBC29857524F CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1062;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 298 VASTSPE 304
Db 604 VASTSPE 610
Search completed: August 3, 2004, 09:09:54
Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:06:52 ; Search time 39 Seconds

(without alignments)
3365.527 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 416

Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKQMPGCFNFKKLFFKTS 416

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriapi.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	6.7	393	11	Q9R0S9
2	28	6.7	453	11	Q8C3Q0
3	28	6.7	454	11	Q9JHK1
4	28	6.7	454	11	Q9R0T0
5	28	6.7	454	11	Q8C3Q9
6	26	6.2	383	11	Q99M88
7	20	4.8	177	11	Q920G4
8	20	4.8	229	11	Q7TQC1
9	17	4.1	403	13	Q90WU0
10	11	2.6	280	13	Q8JGM9
11	11	2.6	280	13	Q8JG42
12	11	2.6	280	13	Q8JIS9
13	11	2.6	282	13	Q98JI8
14	11	2.6	283	13	Q93417
15	11	2.6	290	13	Q8JIS8
16	11	2.6	293	5	Q8I9V7

RESULT 1

Q9R0S9 PRELIMINARY; PRT; 393 AA.

ID Q9R0S9
AC Q9R0S9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Caspase9S.
GN CASP9.

ALIGNMENTS

17	11	2.6	299	5	Q8I955
18	11	2.6	318	13	Q9IB65
19	11	2.6	400	5	Q8ITP2
20	10	2.4	303	11	Q88550
21	10	2.4	308	5	Q9NH99
22	10	2.4	308	5	Q9VET9
23	10	2.4	476	13	Q9IBJ3
24	10	2.4	520	13	Q9IB62
25	10	2.4	522	4	Q8IUP5
26	9	2.2	370	5	Q22518
27	9	2.2	481	11	Q812G4
28	9	2.2	1121	10	Q942F3
29	9	2.2	1164	10	Q9LJF3
30	8	1.9	145	9	Q8LRT5
31	8	1.9	158	10	Q8H436
32	8	1.9	165	17	Q970W7
33	8	1.9	266	16	Q82TV7
34	8	1.9	272	16	Q7V7P6
35	8	1.9	272	16	Q7U6Q4
36	8	1.9	324	16	Q8YAX5
37	8	1.9	368	16	Q9XAC4
38	8	1.9	372	16	Q9KUW7
39	8	1.9	378	16	Q8FXG8
40	8	1.9	399	13	Q9IB63
41	8	1.9	415	13	Q801M6
42	8	1.9	419	13	Q7ZXD2
43	8	1.9	423	13	Q9IB67
44	8	1.9	618	2	Q8KFX0
45	8	1.9	752	5	Q21026
46	8	1.9	758	5	Q22203
47	8	1.9	787	10	Q48847
48	8	1.9	794	5	Q18107
49	8	1.9	975	5	Q9VAX8
50	8	1.9	1031	5	Q962H8
51	8	1.9	1393	16	Q822J2
52	8	1.9	1791	16	Q8ABE6
53	7	1.7	87	9	Q854Q9
54	7	1.7	91	2	Q9EXM1
55	7	1.7	93	16	Q7UT81
56	7	1.7	98	16	Q8YLM1
57	7	1.7	111	2	Q924C6
58	7	1.7	116	4	Q725Z7
59	7	1.7	121	11	Q8BG00
60	7	1.7	121	16	Q89SC1
61	7	1.7	123	2	Q9ZAN6
62	7	1.7	126	8	Q9B4Y3
63	7	1.7	129	5	Q9N9C1
64	7	1.7	131	10	Q7XQY4
65	7	1.7	135	2	Q53304
66	7	1.7	138	16	Q8EQK6
67	7	1.7	141	10	Q9S7T2
68	7	1.7	143	9	Q857D0
69	7	1.7	143	16	Q83DN9
70	7	1.7	152	16	Q7U4I3
71	7	1.7	153	12	Q91MM8
72	7	1.7	153	12	Q8UTP4
73	7	1.7	153	12	Q8JUT3
74	7	1.7	156	13	Q7ZW78
75	7	1.7	156	16	Q8DC79

Q8I955 spodoptera
Q9IB65 xenopus lae
Q8ITP2 branchiosto
Q88550 rattus norv
Q9NH99 drosophila
Q9VET9 drosophila
Q9IBJ3 brachydanio
Q9IB62 xenopus lae
Q8IUP5 homo sapien
Q22518 caenorhabdi
Q812G4 mus musculu
Q942F3 oryza sativ
Q9LJF3 arabidopsis
Q8LRT5 vibriophag
Q8H436 oryza sativ
Q970W7 sulfolobus
Q82TV7 nitrosomona
Q7V7P6 prochloroco
Q7U6Q4 synechococc
Q8YAX5 streptomyce
Q9XAC4 streptomyce
Q9KUW7 vibrio chol
Q8FXG8 brucella su
Q9IB63 xenopus lae
Q801M6 xenopus lae
Q7ZXD2 xenopus lae
Q9IB67 xenopus lae
Q8KFX0 saccharopol
Q21026 caenorhabdi
Q22203 caenorhabdi
Q48847 arabidopsis
Q18107 caenorhabdi
Q9VAX8 drosophila
Q962H8 toxoplasma
Q822J2 chlamydomphi
Q8ABE6 bacteroides
Q854Q9 mycobacteri
Q9EXM1 escherichia
Q7UT81 rhodospirell
Q8YLM1 anabaena sp
Q924C6 salmonella
Q725Z7 homo sapien
Q8BG00 mus musculu
Q89SC1 bradyrhizob
Q9ZAN6 comamonas s
Q9B4Y3 graomys gri
Q9N9C1 leishmania
Q7XQY4 oryza sativ
Q53304 mycoplasma
Q8EQK6 oceanobacil
Q9S7T2 oryza sativ
Q857D0 mycobacteri
Q83DN9 coxiella bu
Q7U4I3 synechococc
Q91MM8 lumpy skin
Q8JUT3 lumpy skin
Q7ZW78 brachydanio
Q8DC79 vibrio vuln

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
RT caspase-9.";
RL Biochem. Biophys. Res. Commun. 264:550-555(1999).
DR EMBL; AB019601; BAAB6896.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; Peptidase_C14; 1.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02026; CASPASE_P20; 1.
DR NON TER 1
SQ SEQUENCE 393 AA; 42975 MW; CA889475E50DD632 CRC64;

Query Match 6.7%; Score 28; DB 11; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 CPSLGGKPKLFFFIQACGGEQKDHGFEVA 299
Db 310 CPSLGGKPKLFFFIQACGGEQKDHGFEVA 337

RESULT 2
Q8C3Q0 PRELIMINARY; PRT; 453 AA.
AC Q8C3Q0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Caspase 9 (fragment).
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK085152; BAC39378.1; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.

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DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; Peptidase_C14; 1.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR NON TER 1
SQ SEQUENCE 453 AA; 49847 MW; 8F7D1C50F7ABA68F CRC64;

Query Match 6.7%; Score 28; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 CPSLGGKPKLFFFIQACGGEQKDHGFEVA 299
Db 309 CPSLGGKPKLFFFIQACGGEQKDHGFEVA 336

RESULT 3
Q9JHK1 PRELIMINARY; PRT; 454 AA.
AC Q9JHK1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-9 (Caspase-9 long isoform).
GN RNCASP9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY;
RX Cao G., Chen D., Pei W., O'Horo C., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY;
RX Itch T., Itoh A., Pleasure D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RX Cao G., Chen D., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RX Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RX Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RT Apoptosis.";
RL J. Biol. Chem. 276:12190-12200(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=WKY;
RX MEDLINE=21552993; PubMed=11695991;
RX Nishiyama J., Yi X., Venkatachalam M.A., Dong Z.;
RT "cDNA cloning and promoter analysis of rat caspase-9.";

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[illegible]

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RESULT 6
Q99M88 PRELIMINARY; PRT; 383 AA.
AC Q99M88,
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-9 CTD isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RT Apoptosis.";
RL J. Biol. Chem. 276:12190-12200 (2001).
DR EMBL; AY008275; AAC21690.1; -.
DR HSP; P42574; IPAU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILLBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
SQ SEQUENCE 383 AA; 43319 MW; 3C5D217C3100FF25 CRC64;

Query Match 6.2%; Score 26; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 VVILSHGCGQASHLPFGAVYGTDC 256
Db 269 VVILSHGCGQASHLPFGAVYGTDC 294

RESULT 7
Q920G4 PRELIMINARY; PRT; 177 AA.
AC Q920G4,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Caspase-9 short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Chen D., Ma L., Graham S.H., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293333; AAK97066.1; -.

RESULT 8
Q7TQCI PRELIMINARY; PRT; 229 AA.
AC Q7TQCI,
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 25 kDa caspase-9 dominant negative protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Wu S., Sheng L., Graham S.H., Zhou Z., Chen J.;
RT "Molecular cloning and characterization of three caspase-9 dominant
RT negative forms in rats.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV124461; AAM92272.1; -.
DR EMBL; AV124461; AAM92272.1; -.
SQ SEQUENCE 229 AA; 25194 MW; 87C293AF139F3B23 CRC64;

Query Match 4.8%; Score 20; DB 11; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 MIEDIQAGSGSRDQARQL 58
Db 39 MIEDIQAGSGSRDQARQL 58

RESULT 9
Q90WU0 PRELIMINARY; PRT; 403 AA.
AC Q90WU0,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgman J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005486; F:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
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DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS02009; CARD; 1.
SQ SEQUENCE 177 AA; 19700 MW; E9DCDA77156AD748 CRC64;

Query Match 4.8%; Score 20; DB 11; Length 177;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 MIEDIQAGSGSRDQARQL 58
Db 39 MIEDIQAGSGSRDQARQL 58

RESULT 8
Q7TQCI PRELIMINARY; PRT; 229 AA.
AC Q7TQCI,
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 25 kDa caspase-9 dominant negative protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Wu S., Sheng L., Graham S.H., Zhou Z., Chen J.;
RT "Molecular cloning and characterization of three caspase-9 dominant
RT negative forms in rats.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV124461; AAM92272.1; -.
DR EMBL; AV124461; AAM92272.1; -.
SQ SEQUENCE 229 AA; 25194 MW; 87C293AF139F3B23 CRC64;

Query Match 4.8%; Score 20; DB 11; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 MIEDIQAGSGSRDQARQL 58
Db 39 MIEDIQAGSGSRDQARQL 58

RESULT 9
Q90WU0 PRELIMINARY; PRT; 403 AA.
AC Q90WU0,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgman J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005486; F:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
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DR GO: GO:0006915; P:apoptosis; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR InterPro: IPR001193; Mitoch_carrier.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR PROSITE: PS00215; MITOCH_CARRIER; 1.
 FT NON TER 1
 SQ SEQUENCE 403 AA; 44913 MW; 0F1B40C3E6594FC4 CRC64;

Query Match 4.3%; Score 17; DB 13; Length 403;
 Best Local Similarity 100.0%; Pred. No. 9.7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQACGGEQXD 293
 Db 264 GKPKLFFFIQACGGEQXD 280

RESULT 10
 Q8JGM9 PRELIMINARY; PRT; 280 AA.
 AC Q8JGM9;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Caspase 3-like.
 GN CASP3.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hewitt J.E., Bolland D.J.;
 RT "Sequence comparisons of an evolutionary chromosomal breakpoint in human, mouse and pufferfish";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A102865; AAM48291.1; -;
 DR GO: GO:0030693; F:caspase activity; IEA.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 280 AA; 30538 MW; 4D58912159A37347 CRC64;

Query Match 2.6%; Score 11; DB 13; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQAC 287
 Db 159 GKPKLFFFIQAC 169

RESULT 11
 Q8JG42 PRELIMINARY; PRT; 280 AA.
 AC Q8JG42;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Caspase 3.
 GN CASP3.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grewal P.K., van Deutekom J.C., Mills K.A., Lemmers R.J., Mathews K.D., Frants R.R., Hewitt J.E.;
 RT "The mouse homolog of FRG1, a candidate gene for FSHD, maps proximal to the myodystrophy mutation on chromosome 8";
 RL Mamm. Genome 8:394-398(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Grewal P.K., Todd L.C., van der Maarel S., Frants R.R., Hewitt J.E.;
 RT "FRG1, a gene in the FSH muscular dystrophy region on human chromosome 4q35, is highly conserved in vertebrates and invertebrates";
 RL Gene 216:13-19(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Bolland D.J., Hewitt J.E.;
 RT "Intron loss in the SART1 genes of Fugu rubripes and Tetraodon nigroviridis";
 RL Gene 271:43-49(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Bolland D.J., van Geel M., Carim Todd L., Grewal P.K., Beck A.F., van der Maarel M. Sr., Frants R.R., de Jong P.J., Hewitt J.E.;
 RT "Sequence comparisons of an Evolutionary Chromosomal Breakpoint in Human, Mouse and Puffer Fish";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF042797; AAM43816.1; -;
 DR GO: GO:0030693; F:caspase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 280 AA; 30524 MW; 4F2D91245A7EC642 CRC64;

Query Match 2.6%; Score 11; DB 13; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQAC 287
 Db 159 GKPKLFFFIQAC 169

RESULT 12
 Q8JIS9 PRELIMINARY; PRT; 280 AA.
 AC Q8JIS9;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3B.
OS Erythras latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20211495; PubMed=10747068;
RA Naruse K., Fukumachi S., Mitani H., Kondo M., Matsuoka T., Kondo S.,
RA Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
RA Wada H., Kusakabe T., Suzuki N., Kinoshita M., Kanamori A., Terado T.,
RA Kimura H., Nonaka M., Shima A.;
RT "A Detailed Linkage Map of Medaka, Oryzias latipes: Comparative
RT Genomics and Genome Evolution.";
RL Genetics 154:1773-1784(2000).
DR EMBL; AB032608; BAC00948.1; -
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 280 AA; 31168 MW; 5095512F1E485542 CRC64;

Query Match 2.6%; Score 11; DB 13; Length 280;
Best Local Similarity 100.0%; Pred.No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFFIQAC 287
Db 160 GKPKLFFFIQAC 170
|||||

RESULT 13
Q98UI8 PRELIMINARY; PRT; 282 AA.
AC Q98UI8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
GN CASP3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RN SEQUENCE FROM N.A.
RA Yabu T., Okazaki T., Yamashita M.;
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
RT Mammalian Caspase-3.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047003; BAB32409.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR ZFIN; ZDB-GENE-011210-1; casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932B CRC64;

Query Match 2.6%; Score 11; DB 13; Length 282;
Best Local Similarity 100.0%; Pred.No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFFIQAC 287
Db 156 GKPKLFFFIQAC 166
|||||

RESULT 14
O93417 PRELIMINARY; PRT; 283 AA.
AC O93417;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20149872; PubMed=10684799;
RA Johnson A.L., Bridgham J.T.;
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells.";
RL Biol. Reprod. 62:589-598(2000).
DR EMBL; AF083029; AAC32602.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 2.6%; Score 11; DB 13; Length 283;
Best Local Similarity 100.0%; Pred.No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFFIQAC 287
Db 161 GKPKLFFFIQAC 171
|||||

RESULT 15
Q8JIS8 PRELIMINARY; PRT; 290 AA.
AC Q8JIS8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20211495; PubMed=10747068;
RA Naruse K., Fukamachi S., Mitani H., Kondo M., Matsuoka T., Kondo S.,
RA Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
RA Wada H., Kusakabe T., Suzuki N., Kinoshita M., Kanamori A., Terado T.,
RA Kimura H., Nonaka M., Shima A.,
RA "A Detailed Linkage Map of Medaka, Oryzias latipes: Comparative
RT Genomics and Genome Evolution.";
RL Genomics 154:1773-1784(2000).
DR EMBL; AB032609; BAC00949.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 290 AA; 32686 MW; D8C3BC00D32E8A6C CRC64;

Query Match          2.6%; Score 11; DB 13; Length 290;
Best Local Similarity 100.0%; Pred.No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287
DB 166 GKPKLFFIQAC 176

RESULT 16
QY 277 GKPKLFFIQAC 287
DB 166 GKPKLFFIQAC 176

ID Q819V7 PRELIMINARY; PRT; 293 AA.
AC Q819V7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-1.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22358983; PubMed=12324475;
RA Pei Z., Reske G., Huang Q., Hammock B.D., Qi Y., Chejanovsky N.;
RT "Characterization of the Apoptosis Suppressor Protein P49 from the
RT Spodoptera littoralis Nucleopolyhedrovirus.";
RL J. Biol. Chem. 277:48677-48684(2002).
DR EMBL; AF448494; AA86250.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 293 AA; 33340 MW; 8184A9FD910D7E34 CRC64;
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Query Match          2.6%; Score 11; DB 5; Length 293;
Best Local Similarity 100.0%; Pred.No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287
DB 165 GKPKLFFIQAC 175

RESULT 17
QY 277 GKPKLFFIQAC 287
DB 165 GKPKLFFIQAC 175

ID Q819S5 PRELIMINARY; PRT; 299 AA.
AC Q819S5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Effector caspase.
OS Spodoptera littoralis (Egyptian cotton leafworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyridae; Spodoptera.
OX NCBI_TaxID=7109;
RN [1]_
RP SEQUENCE FROM N.A.
RA Liu Q., Gershburg E., Qi Y., Chejanovsky N.;
RT "Suppression of apoptosis in Spodoptera littoralis SL2 cells by the
RT baculovirus proteins P35 and P49.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548387; AA016241.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 299 AA; 33442 MW; B13AF2C1A6BD409D CRC64;

Query Match          2.6%; Score 11; DB 5; Length 299;
Best Local Similarity 100.0%; Pred.No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287
DB 168 GKPKLFFIQAC 178

RESULT 18
QY 277 GKPKLFFIQAC 287
DB 168 GKPKLFFIQAC 178

ID Q91B65 PRELIMINARY; PRT; 318 AA.
AC Q91B65;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-7.
DE CASPASE-7.
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
```

RL J. Biol. Chem. 275:10484-10491 (2000).

DR EMBL; AB0381170; BAA94748.1; --

DR HSSP; P42574; 1PAU.

DR MEROPS; C14.004; --

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; 1.

DR PRINTS; PR00376; IL1BCENZYM.

DR SMART; SM00115; CASC; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS50207; CASPASE_P10; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.

SQ SEQUENCE 318 AA; 35397 MW; 6EBC6684AF86A128 CRC64;

Query Match 2.6%; Score 11; DB 13; Length 318;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287

Db 187 GKPKLFFIQAC 197

RESULT 19

Q8ITP2

ID Q8ITP2

AC Q8ITP2; PRELIMINARY; PRT; 400 AA.

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE AmphicASP-6.

OS Branchiostoma floridae (Florida lancelet) (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

OC Branchiostoma.

OX NCBI_TaxID=7739;

[1]

SEQUENCE FROM N.A.

RA Bayasas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,

Comella J.X.;

RT "Isolation of AmphicASP-6, an amphioxus (Branchiostoma floridae)

RT caspase-6 homolog containing a Pyrin prodomain."

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF412336; AAN45850.1; --

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE_p20.

DR Pfam; PF00656; Peptidase C14.

DR PRINTS; PR00376; IL1BCENZYM.

DR SMART; SM00115; CASC; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS50207; CASPASE_P10; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.

SQ SEQUENCE 400 AA; 44309 MW; 5C3B1B813E73DFAE CRC64;

Query Match

Best Local Similarity 2.6%; Score 11; DB 5; Length 400;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287

Db 260 GKPKLFFIQAC 270

RESULT 20

O88550

ID O88550

PRELIMINARY; PRT; 303 AA.

O88550;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Caspase-7.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Forghani F., Roy S.;

RT "Rat caspase-7 sequence."

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF072124; AAC24011.1; --

DR HSSP; P42574; 1PAU.

DR MEROPS; C14.004; --

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE_p20.

DR Pfam; PF00656; Peptidase C14.

DR PRINTS; PR00376; IL1BCENZYM.

DR SMART; SM00115; CASC; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS50207; CASPASE_P10; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.

SQ SEQUENCE 303 AA; 34324 MW; A71728754BFF19DD CRC64;

Query Match

Best Local Similarity 2.4%; Score 10; DB 11; Length 303;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287

Db 177 KPKLFFIQAC 186

RESULT 21

Q9NH9

ID Q9NH9

AC Q9NH9; PRELIMINARY; PRT; 308 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Caspase 6-like protein BG2.

GN DRCAY OR CGI4902.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhou L., Steller H.;

RT "BG2, a potential Drosophila homologue of Caspase 6."

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF222007; AAF44327.1; --

DR HSSP; P42574; 1PAU.

DR MEROPS; C14.022; --

DR FlyBase; FBgn0028381; decay.

DR GO; GO:0005737; C:cytoplasm; IDA.

DR GO; GO:0004208; F:caspase-3 activity; IDA.

DR GO; GO:0004207; F:effector caspase activity; NAS.

DR GO; GO:0006915; P:apoptosis; IMP.

DR InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE_p20.

DR Pfam; PF00656; Peptidase C14.

DR PRINTS; PR00376; IL1BCENZYM.

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DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50209; CASPASE_P20; 1.
SQ SEQUENCE 308 AA; 34897 MW; E3FDAB05FEC7E93 CRC64;

Query Match 2.4%; Score 10; DB 5; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 162 KPXLFFFIQAC 171

RESULT 22
Q9VET9
ID Q9VET9 PRELIMINARY; PRT; 308 AA.
AC Q9VET9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Decay protein (AT03047p).
GN DSCAY OR CG14902.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Nephroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levinsoy A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99452973; PubMed=10521468;
RA Dorstyn L., Read S.H., Quinn L.M., Richardson H., Kumar S.;
RT "DECAY, a novel Drosophila caspase related to mammalian caspase-3 and
RT caspase-7.";
RL J. Biol. Chem. 274:30778-30783(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Dorstyn L., Read S.H., Kumar S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavetz C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003713; AAF55329.1; -.
DR EMBL; AF130469; AAD54071.2; -.
DR EMBL; AY089242; AAL89980.1; -.
DR HSP; P42574; IPAU.
DR MEROPS; C14.022; -.
DR FlyBase; FBgn0028381; decay.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0004208; F:caspase-3 activity; IDA.
DR GO; GO:0004207; F:effector caspase activity; NAS.
DR GO; GO:0006915; P:apoptosis; IMP.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 308 AA; 34911 MW; 686DA39060EC78C1 CRC64;

Query Match 2.4%; Score 10; DB 5; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 162 KPXLFFFIQAC 171

RESULT 23
Q918J3
ID Q918J3 PRELIMINARY; PRT; 476 AA.
AC Q918J3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-8.
GN CASP8
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF273220; AAF79207.1; -.
DR HSP; Q15806; IQDU.

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RC STRAIN=Bristol N2;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "The C. elegans genome project: Contiguous nucleotide sequence of over
 RT two megabases from chromosome III.";
 RL Nature 0:0-0(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Taich A.;
 RL "The sequence of C. elegans cosmid T15B12.";
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U14634; AAA21560.1; -;
 DR PIR; B88455; B88455.
 DR HSP; Q06486; ICKJ.
 DR WormPep; T15B12.2; CE01404.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR00719; Prot_kinase
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; pkinase; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 370 AA; 42308 MW; A485A/DCC6F57599 CRC64;

 Query Match 2.2%; Score 9; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 131 IGSFGFGDV 139
 Db 57 IGSFGFGDV 65

 RESULT 27
 Q812G4 PRELIMINARY; PRT; 481 AA.
 ID Q812G4;
 AC Q812G4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CASP8 and FADD-like apoptosis regulator.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029223; AAH29223.1; -;
 DR GO; GO:0016323; F:apoptosis regulator activity; IEA.
 DR GO; GO:0030693; F:caspace activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR SMART; SM00115; CASC; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS0168; DED; 2.
 SQ SEQUENCE 481 AA; 54874 MW; 433E07E2E5FA5A05 CRC64;

 Query Match 2.2%; Score 9; DB 11; Length 481;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 277 GKPKLFFIQ 285
 Db 352 GKPKLFFIQ 360

 RESULT 28
 Q942F3 PRELIMINARY; PRT; 1121 AA.
 ID Q942F3
 AC Q942F3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative brassinosteroid-insensitive protein BR11.
 GN P0480C01.13.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0480C01.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AP003453; BAB68053.1; -;
 DR Gramene; Q942F3; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00560; LRR; 15.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1121 AA; 120180 MW; F71A49B45E0E2D09 CRC64;

 Query Match 2.2%; Score 9; DB 10; Length 1121;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 131 IGSFGFGDV 139
 Db 813 IGSFGFGDV 821

 RESULT 29

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Q9LJF3
ID Q9LJF3 PRELIMINARY; PRT; 1164 AA.
AC Q9LJF3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor protein kinase (AT3g13380/MRP15_1).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RV [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221 (2000).
RV [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.;
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kaniya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.W., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB000603; BAB01743.1; -.
DR EMBL; AY128280; AAM91089.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 15.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1164 AA; 126660 MW; 79380581D400EEC CRC64;

Query Match 2.2%; Score 9; DB 10; Length 1164;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSGGFGDV 139
Db 864 IGSGGFGDV 872

RESULT 30
Q8LT85
ID Q8LT85 PRELIMINARY; PRT; 145 AA.
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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AC Q8LT85;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Vibrio phage Vp262.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=194802;
RN [1]
RP SEQUENCE FROM N.A.
RA Hardies S.C.;
RT "The complete sequence of Vibriophage VpV 262.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY095314; AAM28362.1; -.
KW Hypothetical protein.
SQ SEQUENCE 145 AA; 16341 MW; 79B9720F88C1B998 CRC64;

Query Match 1.9%; Score 8; DB 9; Length 145;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LARQDHGA 226
Db 14 LARQDHGA 21

RESULT 31
Q8H436
ID Q8H436 PRELIMINARY; PRT; 158 AA.
AC Q8H436;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P0407H12.33 protein.
GN P0407H12.33.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0407H12.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004303; BAC21455.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001209; Ribosomal S14.
DR PROSITE; PS00527; RIBOSOMAL S14; 1.
SQ SEQUENCE 158 AA; 17275 MW; AAD0FB7B5BA02983 CRC64;

Query Match 1.9%; Score 8; DB 10; Length 158;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LRRCLRL 16
Db 54 LRRCLRL 51

RESULT 32
Q970W7
ID Q970W7 PRELIMINARY; PRT; 165 AA.
AC Q970W7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Hypothetical protein ST1485.
GN ST1485.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000986; BAB66556.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 165 AA; 19200 MW; 4A39578B3CCA2400 CRC64;

Query Match 1.9%; Score 8; DB 17; Length 165;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALESRLGN 148
Db 99 ALESRLGN 106
|||||

RESULT 33
Q82TY7 PRELIMINARY; PRT; 266 AA.
AC Q82TY7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created);
DI 01-JUN-2003 (TrEMBLrel. 24, Last sequence update);
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update);
DE DUF173.
GN NEI1728.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321862; CAD85639.1; --
DR InterPro; IPR003768; DUF173.
DR Pfam; PF02616; DUF173; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30676 MW; 2E34DBA9452EA1DB CRC64;

Query Match 1.9%; Score 8; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELAR 221
Db 233 LALLELAR 240
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RESULT 34
Q7V7P6 PRELIMINARY; PRT; 272 AA.
ID Q7V7P6
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AC Q7V7P6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created);
DI 01-OCT-2003 (TrEMBLrel. 25, Last sequence update);
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update);
DE ABC transporter component, likely for sugar transport precursor.
GN PWT0892.
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Stiglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572097; CAE20867.1; --
KW Signal; Sugar transport; Complete proteome.
FT SIGNAL 1 36 Potential.
SQ SEQUENCE 272 AA; 30157 MW; 5FE29ECA6855EA6 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 272;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELAR 221
Db 117 LALLELAR 124
|||||

RESULT 35
Q7U6Q4 PRELIMINARY; PRT; 272 AA.
AC Q7U6Q4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created);
DI 01-OCT-2003 (TrEMBLrel. 25, Last sequence update);
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update);
DE ABC transporter, likely for trehalose/maltose, membrane component
DE precursor.
GN SYNW1284.
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569692; CAE07799.1; --
KW Signal; Complete proteome.
FT SIGNAL 1 32 Potential.
SQ SEQUENCE 272 AA; 30051 MW; CODFDCFBA7B5D9E CRC64;

Query Match 1.9%; Score 8; DB 16; Length 272;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELAR 221
Db 117 LALLELAR 124
|||||

RESULT 36
Q8YAX5 PRELIMINARY; PRT; 324 AA.
ID Q8YAX5
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AC Q8YAX5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Oxidoreductase (EC 1.1.1.-).
 GN BMEI11126.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kaparatil V., Redkar R.J., Patra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonks L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kypides N., Overbeek R.,
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 RL EMBL; AE009744; AAL54368.1; -.
 DR PIR; AE3650; AE3650.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000683; GFO_IDH_MCCA.
 DR Pfam; PF01408; GFO_IDH_MCCA; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 324 AA; 35683 MW; 3817F85ABDA4112 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 324;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARQ 222
 |||||
 DB 103 ALLELARQ 110

RESULT 37

Q9XAC4
 ID Q9XAC4 PRELIMINARY; PRT; 368 AA.
 AC Q9XAC4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein SCO1932.
 GN SCO1932 OR SCC22.14C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AJ939110; CAB50757.1; -.
 DR PIR; T36004; T36004.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Peptidase S8.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 368 AA; 38767 MW; DBF94549F6303FF0 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 368;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EADRLRLR 10
 |||||
 DB 81 EADRLRLR 88

RESULT 38

Q9KUW7
 ID Q9KUW7 PRELIMINARY; PRT; 372 AA.
 AC Q9KUW7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aminotransferase, class V.
 GN VC0392.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004127; AAF93565.1; -.
 DR PIR; G82328; G82328.
 DR TIGR; VC0392; -.
 DR GO; GO:0008483; F:transaminase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR000192; Aminotrans_V.
 DR Pfam; PF0266; aminotran_5; 1.
 DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 372 AA; 40623 MW; 00D5AFD1B6F6947B CRC64;

Query Match 1.9%; Score 8; DB 16; Length 372;

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Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GCPVSVEX 262
Db 119 GCPVSVEX 126
|||||

RESULT 39
Q8FXG8 PRELIMINARY; PRT; 378 AA.
AC Q8FXG8
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Oxidoreductase, Gfo/Idh/MocA family.
GN BRA0109.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AS014514; AAN33319.1; -.
DR TIGR; BRA0109; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000683; GFO_IDH_MocA.
DR Pfam; PF01408; GFO_IDH_MocA; 1.
KW Complete proteome.
SQ SEQUENCE 378 AA; 41413 MW; 7F53CB86065F3787 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 378;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARQ 222
Db 103 ALLELARQ 110
|||||

RESULT 40
Q9IB63 PRELIMINARY; PRT; 399 AA.
AC Q9IB63
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).

EMBL; AB038172; BAA94750.1; -.
HSP; Q15806; 1QDU.
MEROPS; C14.010; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0030693; F:caspase activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR001315; CARD.
InterPro; IPR004488; Death.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; ILIBENZIME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS02029; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS02027; CASPASE_P10; 1.
PROSITE; PS02028; CASPASE_P20; 1.
PROSITE; PS00017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match 1.9%; Score 8; DB 13; Length 399;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 LETRGSQA 69
Db 60 LETRGSQA 67
|||||

RESULT 41
Q801M6 PRELIMINARY; PRT; 415 AA.
AC Q801M6
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049286; AAH49286.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001315; CARD.
InterPro; IPR001309; ICE_p20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; ILIBENZIME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS02029; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS02028; CASPASE_P20; 1.
KW Hypothetical protein.
```

SQ SEQUENCE 415 AA; 46542 MW; CD253432B40BE58B CRC64;
Query Match. 1.9%; Score 8; DB 13; Length 415;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 248 GAVYGTGDG 255
Db 245 GAVYGTGDG 252
RESULT 42
ID Q7ZXD2 PRELIMINARY; PRT; 419 AA.
AC Q7ZXD2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045046; AAI45046.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SMC0114; CARD; 1.
DR SMART; SMC0115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 419 AA; 46900 MW; 6EF6AAC592CAF65D CRC64;
Query Match. 1.9%; Score 8; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 248 GAVYGTGDG 255
Db 249 GAVYGTGDG 256
RESULT 43
ID Q9IB67 PRELIMINARY; PRT; 423 AA.
AC Q9IB67;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-2.
GN XCASPASE-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

Query Match. 1.9%; Score 8; DB 13; Length 423;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 248 GAVYGTGDG 255
Db 249 GAVYGTGDG 256
RESULT 44
ID Q8KFX0 PRELIMINARY; PRT; 618 AA.
AC Q8KFX0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Methylmalonyl-CoA mutase, small subunit.
GN MUTA.
OS Saccharopolyspora erythraea (Streptomyces erythraeus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Saccharopolyspora.
OX NCBI_TaxID=1836;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA340;
RA Iuz-Madrigal A., Petrosyan P., De la Torre P., Flores M.E.;
RT "Saccharopolyspora erythraea genomic DNA comprising methylmalonyl-CoA
mutase operon."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY117133; AAM77044.1; -.
DR GO; GO:0004494; F:methylmalonyl-CoA mutase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006099; MMCoA mutase.
DR Pfam; PF01642; MM_CoA mutase; 1.
SQ SEQUENCE 618 AA; 66044 MW; 7BE8E3B3A4D91CBE1 CRC64;
Query Match. 1.9%; Score 8; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 360 GSWYVETL 367

Db 386 GSWYVETL 393

RESULT 45

T201026	ID	Q201026		PRT;	752 AA.
	AC	PRELIMINARY;			
	DC	Q201026;			
	DT	01-NOV-1996	(TREMBLrel. 01, Created)		
	DD	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
	DE	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
	DE	F59A6.4	protein.		
	GN	F59A6.4.			
	OS	Caeenorhabditis elegans.			
	OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;			
	CC	Rhabditidae; Peloderinae; Caeonorhabditis.			
	NX	NCBI_TaxID=6239;			
	QN	[1]			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN=Bristol NZ;			
	FX	MEDLINE=99069613; PubMed=9851916;			
	RA	Note:			
	RT	"Genome sequence of the nematode C. elegans: a platform for			
	RT	investigating biology. The C. elegans Sequencing Consortium."			
	RL	Science 282:2012-2018(1998).			

RESULT 46

Q22203	PRELIMINARY;	PRT;	758 AA.
ID	Q22203		
AC	Q22203;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Hypothetical protein.		
GN	T0547.6		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI TaxID=6239;		

RESULT 47

AD 048847 PRELIMINARY; PRT; 787 AA.
 IC O48847;
 ID O48847;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE F24L7.16 protein (AF23G2700/F24L7.16).
 GN F24L7.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RC Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
 RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
 RA Somerville C.R., Venter J.C.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
 RA Bowler L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Sato M.,
 RA Schenck C., Shigenaga Y., Shinozaki K., Suganuma T., Tamada K.,

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RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones." to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones." to the EMBL/GenBank/DBJ databases.
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC003974; AAC04493.1; -.
DR EMBL; AF367306; AAK32893.1; -.
DR EMBL; BT002219; AAN72230.1; -.
DR PIR; T00798; T00798.
DR InterPro; IPR001680; WD40.
DR Pfam; PF004400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00667; Lish; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50896; LISH; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00882; WD_REPEATS_2; 5.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 787 AA; 85514 MW; 995B52584090CEC3 CRC64;

Query Match 1.9%; Score 8; DB 10; Length 787;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 FGDVGALE 143
Db 456 FGDVGALE 463
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RESULT 48
ID O18107 PRELIMINARY; PRT; 794 AA.
AC O18107; 062283;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE H05L14.1 protein.
GN H05L14.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonnenhammer B., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
```

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RL Nature 368:32-38 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RA McMurray A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99772; CABI6921.1; -.
DR EMBL; Z75550; CABI6921.1; JOINED.
DR EMBL; Z75550; CAA99932.1; -.
DR EMBL; Z99772; CAA99932.1; JOINED.
DR PIR; T23048; T23048.
DR HSSP; Q06486; ICKI.
DR WormPep; H05L14.1; CE16168.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 2.
DR ProDom; PD000001; Prot_kinase; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
KW ATP-binding; Transferase.
SQ SEQUENCE 794 AA; 89743 MW; 8595E1971334DD9C CRC64;

Query Match 1.9%; Score 8; DB 5; Length 794;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGFGDGV 139
Db 468 GSGFGDGV 475
|||||

RESULT 49
Q9VAX8 PRELIMINARY; PRT; 975 AA.
ID Q9VAX8
AC Q9VAX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG4849 protein (LD28793p).
GN CG4849.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertis J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weissbach G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guanin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003763; AAF56769.1; -;
DR EMBL; AY089551; AAL90289.1; -;
DR FlyBase; FBgn0039566; CG4849.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR000640; EFG.C.
DR InterPro; IPR009022; EFG-III.V.
DR InterPro; IPR005517; EFG-IV.
DR InterPro; IPR004161; EFTU D2.
DR InterPro; IPR000795; EF-GTPbind.
DR InterPro; IPR005225; Small GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW GTP-binding; Protein biosynthesis.
SQ SEQUENCE 975 AA; 110649 MW; 68A9072B3300E9CB CRC64;

Query Match 1.9%; Score 8; DB 5; Length 975;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 LLELARQD 223
Db 961 LLELARQD 968
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RESULT 50
Q962H8 PRELIMINARY; PRT; 1031 AA.
AC Q962H8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Membrane skeleton protein IMC2.
GN IMC2.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;

RX MEDLINE=21313687; PubMed=11420112;
RA Mann T., Beckers C.;
RT "Characterization of the subpellicular network, a filamentous membrane
skeletal component in the parasite *Toxoplasma gondii*.";
RL Mol. Biochem. Parasitol. 115:257-268 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Beckers C.J., Mann T.M.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032682; AAK38356.2; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M-peptidase.
DR Pfam; PF00149; Metallophos; 1.
SQ SEQUENCE 1031 AA; 117427 MW; 9EAB3A0E148BE4F4 CRC64;

Query Match 1.9%; Score 8; DB 5; Length 1031;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 RAGSGSRR 52
Db 777 RAGSGSRR 784
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Job time : 42 secs

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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:15 ; Search time 13 Seconds
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1666.245 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2166	99.4	416	1	ICE9 HUMAN
2	465	21.3	424	1	ICE2 CHICK
3	428	19.6	277	1	ICE3 CRILLO
4	418	19.2	277	1	ICE3 HUMAN
5	418	19.2	277	1	ICE3 MOUSE
6	411	18.3	435	1	ICE2 MOUSE
7	409	18.8	277	1	ICE3 RAT
8	409	18.8	435	1	ICE2 HUMAN
9	407	18.7	496	1	CE03 CAEUVI
10	389.5	17.9	480	1	ICE8 MOUSE
11	387.5	17.8	503	1	CE03 CAEVL
12	383	17.6	479	1	ICE8 HUMAN
13	364.5	16.7	303	1	ICE7 MESAU
14	361.5	16.6	303	1	ICE7 HUMAN
15	350.5	16.1	303	1	ICE7 MOUSE
16	349	16.0	282	1	ICE3 XENLA
17	324	14.9	339	1	ICE DROME
18	322	14.8	276	1	ICE6 MOUSE
19	320	14.7	323	1	ICE1 DROME
20	312.5	14.3	312	1	ICE2 RAT
21	311.5	14.3	293	1	ICE6 HUMAN
22	305	14.0	521	1	ICEA HORSE
23	300.5	13.8	405	1	ICE1 SPORF
24	297.5	13.6	299	1	ICEB XENLA
25	279	12.8	382	1	ICEB XENLA
26	278	12.8	404	1	ILBC PTG
27	274	12.6	410	1	ILBC FELCA
28	270.5	12.4	402	1	ILBC RAT
29	268.5	12.3	402	1	ILBC MOUSE
30	262	12.0	404	1	ILBC CANFA
31	259	11.9	404	1	ILBC HUMAN
32	256	11.7	386	1	ICEA XENLA
33	253	11.6	257	1	ICEE MOUSE

34	239.5	11.0	242	1	ICEE HUMAN
35	232	10.6	377	1	ICED BOVIN
36	212	9.7	373	1	ICE4 MOUSE
37	210	9.6	418	1	ICE5 HUMAN
38	209	9.6	377	1	ICE4 HUMAN
39	207	9.5	419	1	ICEC MOUSE
40	165	7.6	484	1	CFLA MOUSE
41	147	6.7	480	1	CFLA HUMAN
42	113.5	5.2	1612	1	RRPO ORSVS
43	106.5	4.9	589	1	EGPI MOUSE
44	98.5	4.5	915	1	SFBI HUMAN
45	97.5	4.5	382	1	AMAC HUMAN

ALIGNMENTS

RESULT 1
ICE9_HUMAN
ID ICE9_HUMAN STANDARD; PRT; 416 AA.
AC P55211; Q92852; Q9BQ62; Q9UEQ3; Q9UIJ8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic
DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease
DE activating factor 3) (APAF-3).
GN CASP9 OR MCH6.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.
RA Duan H., Orth K., Chimnayan A.M., Poirier G.G., Froelich C.J.,
RA He W.-W., Dixit V.M.;
RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated
RT by the cytotoxic T cell protease granzyme B";
RL J. Biol. Chem. 271:16720-16724 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.
RC TISSUE=T-cell;
RX MEDLINE=97059171; PubMed=8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin beta converting enzyme-like homolog Mch6 and
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
RT mediator CPP32";
RL J. Biol. Chem. 271:27099-27106 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315341; PubMed=10384055;
RA Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P.,
RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;
RT "Genomic organization of the human caspase-9 gene on chromosome
RT 1p36.1-p36.3";
RL Mamm. Genome 10:757-760 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99168502; PubMed=10070954;
RA Srinivasula S.M., Almad M., Guo Y., Zhan Y., Lazebnik Y.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification of an endogenous dominant-negative short isoform of
RT caspase-9 that can regulate apoptosis";
RL Cancer Res. 59:999-1002 (1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Stomach cancer;
RA Izawa M., Mori T., Ito H., Sairenji T.;
RT "Molecular cloning and sequencing of a cDNA predicting an alternative
RT form of pro-caspase-9 from human gastric cancer cell lines.";

```

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN 16]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Miho Y., Momoi T., Fujita E.;
RT "A novel splicing product of human caspase-9 lacking protease
RT activity.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN 17]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT VAL-28.
RX MEDLINE=99107856; PubMed=9890966;
RA Seol D.W., Billiar T.R.;
RT "A caspase-9 variant missing the catalytic site is an endogenous
RT inhibitor of apoptosis.";
RL J. Biol. Chem. 274:2072-2076 (1999).
RN 18]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28; LEU-99; ILE-102;
VAL-106; ASP-114; HIS-173 AND ARG-221.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN 19]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Thomas D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN 110]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Eye, and Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC 1- FUNCTION: Isoform 2 lacks activity is an dominant-negative
CC inhibitor of caspase-9.
CC 1- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.
CC Caspase-9 and APAF1 bind to each other via their respective NH2-
CC terminal CED-3 homologous domains in the presence of cytochrome C
CC and ATP. Interacts with BIRC7.
CC 1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=9L, Alpha;
CC IsoId=P55211-1; Sequence=Displayed;
CC Name=2; Synonyms=9S, Beta;
CC IsoId=P55211-2; Sequence=VSP_000818;
CC 1- TISSUE SPECIFICITY: Ubiquitous, with highest expression in the
CC heart, moderate expression in liver, skeletal muscle, and
CC pancreas. Low levels in all other tissues.
CC 1- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32
CC GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 AND -10 CAN ALSO BE
CC INVOLVED IN THESE PROCESSING EVENTS.
CC 1- SIMILARITY: Belongs to peptidase family C14.

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CC 1- SIMILARITY: Contains 1 CARD domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
EMBL; U56390; AAC50640.1; -
DR EMBL; U60521; AAC50776.1; -
DR EMBL; AB019205; BAA82697.1; -
DR EMBL; AB019197; BAA82697.1; JOINED.
DR EMBL; AB019198; BAA82697.1; JOINED.
DR EMBL; AB019199; BAA82697.1; JOINED.
DR EMBL; AB019200; BAA82697.1; JOINED.
DR EMBL; AB019201; BAA82697.1; JOINED.
DR EMBL; AB019202; BAA82697.1; JOINED.
DR EMBL; AB019203; BAA82697.1; JOINED.
DR EMBL; AB019204; BAA82697.1; JOINED.
DR EMBL; AF093130; AAD12248.1; -
DR EMBL; AB015653; BAA78780.1; -
DR EMBL; AB020979; BAA87905.1; -
DR EMBL; AF110376; AAD13615.1; -
DR EMBL; AL512883; CAC42423.1; -
DR EMBL; AY214168; AAO21133.1; -
DR EMBL; BC002452; AAH02452.1; -
DR EMBL; BC006463; AAH06463.1; -
DR PDB; 3YGS; 19-APR-00.
DR MEROPS; C14.010; -
DR Genew; HGNC:1511; CASP9.
DR MTM; 602234; -
DR GO; GO:0004211; F:caspase-9 activity; TAS.
DR GO; GO:0004937; F:cysteine-type endopeptidase activity; TAS.
DR GO; GO:0008043; F:enzyme activator activity; TAS.
DR GO; GO:0008233; F:peptidase activity; TAS.
DR GO; GO:0008632; P:apoptotic program; TAS.
DR GO; GO:0008635; P:caspase activation via cytochrome c; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW PROPEP 1 ?
KW Polymorphism; 3D-structure.
FT PROPEP 1 315
FT CHAIN ? 315
FT PROPEP 316 330
FT CHAIN 331 416
FT DOMAIN 1 92
FT ACT SITE 237 237
FT ACT SITE 287 287
FT VARSPIC 140 289
FT VARIANT 28 28
FT VARIANT 99 99
FT VARIANT 102 102
FT VARIANT 106 106
FT VARIANT 114 114
FT VARIANT 114 114

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Query Match          99.4%; Score 2166; DB 1; Length 416;
Best Local Similarity 99.3%; Pred. No. 9.4e-177;
Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLVEELQVDQLDVLASFLRNQAGLSKPTLENLTPVVLPEIRKPEV 120
DB 1 MDEADRLRLRCRLVEELQVDQLDVLASFLRNQAGLSKPTLENLTPVVLPEIRKPEV 120
QY 61 DLETRGSOALPLFISCLDGTQDMVLASFLRNQAGLSKPTLENLTPVVLPEIRKPEV 120
DB 61 DLETRGSOALPLFISCLDGTQDMVLASFLRNQAGLSKPTLENLTPVVLPEIRKPEV 120
QY 121 LRPEPRPVIGSGGFDVGALESRLGNADLAYILSMPECGHCLINNVPFCRESGLRTR 180
DB 121 LRPEPRPVIGSGGFDVGALESRLGNADLAYILSMPECGHCLINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRFSLSHFVVKGDLTAKKMWLALLELARQDHGALDCCVWVILSHGCC 240
DB 181 TGSNIDCEKLRRLRFSLSHFVVKGDLTAKKMWLALLELARQDHGALDCCVWVILSHGCC 240
QY 241 ASHLOPFGAVYGTDCGVPVSEKVINIFNGTSCPSLGGKPKLFTIQACGGQKDHGEVAS 300
DB 241 ASHLOPFGAVYGTDCGVPVSEKVINIFNGTSCPSLGGKPKLFTIQACGGQKDHGEVAS 300
QY 301 TSPEDSPGNSNPDPATPFQEGRLTDPDLDALSSLTPTSDIFVSYSTFFGFSWRDPKSG 360
DB 301 TSPEDSPGNSNPDPATPFQEGRLTDPDLDALSSLTPTSDIFVSYSTFFGFSWRDPKSG 360
QY 361 SWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
DB 361 SWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 2
ICE2_CHKCK STANDARD; PRT; 424 AA.
AC Q98943;
RC STRAIN=White leghorn; TISSUE=Ovarian granulosa;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-2 precursor (BC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
DE 1L/1S).
GN CASP2 OR ICH1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
RX MEDLINE=97368127; PubMed=9224894;
RA Johnson A.L., Bridgman J.T., Bergeron L., Yuan J.;
RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary.";
RL Gene 192:227-233(1997).
CC -!- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=ICH-1L;
CC IsoId=Q98943-1; Sequence=Displayed;
CC Note=Only form found in the ovary;
CC Name=ICH-1S;
CC IsoId=Q98943-2; Sequence=VSP_000803, VSP_000804;
CC -!- PTM: Heterodimer of a small and a large subunit (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; U64963; AAC29881.1; ALT_INIT.
HSP; P42574; 1CP3.
MEROPS; C14.006; -.
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IUBCENZYM.
SMART; SM00114; CARD; 1.
SMART; SM00115; CARD; 1.
PROSITE; PS0209; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
FT PROPEP 1 140
FT CHAIN 141 308
FT CHAIN 309 424
FT CHAIN 315 424
FT DOMAIN 7 96
FT ACT_SITE 248 248
FT ACT_SITE 291 291
FT VARSPPLIC 1 7
FT VARSPPLIC 294 424
FT DETDGVDDQDQKERSDPSGCEESDANKEENIKLRLPTRSD
FT MITGVACLGKTAAMRTKSGVIEALTTFVAEDSRDTHVA
FT DMLVKNRQIKOREGVAPGTEFHRCKEMSEYCSLCLDLVL
FT FPGYVPGK -> GVGSIHHLPLCCCHICCSMRGTGEWI
FT REMAKNGOIPQAVRVMQTRKKLSSVCVCLHAPI (in
FT isoform ICH-1S).
FT /FTID=VSP_000804.
SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;

Query Match          21.3%; Score 465; DB 1; Length 424;
Best Local Similarity 30.7%; Pred. No. 6.3e-32;
Matches 128; Conservative 73; Mismatches 172; Indels 44; Gaps 12;

QY 1 MDEADRLRLRCRLVEELQVDQLDVLASFLRNQAGLSKPTLENLTPVVLPEIRKPEV 59
DB 7 MQRVHQEALKKNRVMLARELVKELMEHMEIKDITIEWEMIQAKSGSFQNVFELNI- 65
QY 60 IDLETRGSOALPLFISCLDGTQDMVLASFLRNQAGLSKPTLENLTPVVLPEIRKPEV 114
DB 66 --LPKRGPNFSAFCEALQETKQQLAEMLKTESLRHGIATLEQRYGSNL-PLPL- 119
QY 115 IRKPEVLPRPVPVIGSGGFDVGALESRLGNADLAYILSMPECGHCLINNVPFCRESGLRTR 166
DB 120 --SESCNSKRPRLIVEHSLDSDGPGPIPVKHCTPEFYRHOHLAYILSEPRGLAIL 176
QY 167 NVNVPFCRESGLRTRTGSNIDCEKLRRLRFSLSHFVVKGDLTAKKMWLALLELARQDHG 225
DB 177 SNHIFSEKDLRYRSGGDVDCASLELLFKHLGYQVTFHDSQSAEMESALERFSKLPDHQ 236
QY 226 ALDCVWVILSHGCCQASHLQFPFGAVYGTDCGVPVSEKVINIFNGTSCPSLGGKPKLFFIQ 285
DB 237 DVDSCLVALLSHGVE-----GVGYGTGKLLQLQEAFLFDNANCPNLQNKPMFFIQ 289
QY 286 ACQGEQKDHGEVASSTPEDESGNSNPDPATPFQEGRLTDPDLDALSSLTPTSDIFVSY 345
DB 290 ACRGDETRGVDDQDQKERSDPSGCE-ESDANK-EENIKL-----RUPTRSDMICG 339
QY 346 STFPFGVSWRDPKSGSVYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPG 402

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[5]
 RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
 RC TISSUE=Lymph;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
 RX MEDLINE=95319529; PubMed=7596430;
 RA Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
 RA Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
 RA Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
 RA Miller D.K.;
 RT "Identification and inhibition of the ICE/CED-3 protease necessary
 RT for mammalian apoptosis.";
 RL Nature 376:37-43(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
 RX MEDLINE=96266352; PubMed=8673606;
 RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
 RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
 RA Thornberry N.A., Becker J.W.;
 RT "The three-dimensional structure of apopain/CPP32, a key mediator of
 RT apoptosis.";
 RL Nat. Struct. Biol. 3:619-625(1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
 RX MEDLINE=97197830; PubMed=9045680;
 RA Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
 RA Priestle J.P., Tomaselli K.J., Gruetter M.G.;
 RT "Structure of recombinant human CPP32 in complex with the
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
 RL J. Biol. Chem. 272:6539-6547(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=20283632; PubMed=10821855;
 RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
 RA Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
 RA Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDewitt P.J.,
 RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
 RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
 RT inhibit apoptosis and maintain cell functionality.";
 RL J. Biol. Chem. 275:16007-16014(2000).
 RN [10]
 RP PROCESSING.
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN [11]

RP CLEAVAGE OF HUNTINGTIN.
 RX MEDLINE=96331285; PubMed=8696339;
 RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
 RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
 RA Vaillancourt J.P., Hayden M.R.;
 RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
 RT is modulated by the polyglutamine tract.";
 RL Nat. Genet. 13:442-449(1996).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9. Involved in the
 CC cleavage of huntingtin.
 CC -!- ENZYME REGULATION: Inhibited by isatin sulfonamides.
 CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
 CC and kidney. Moderate levels in brain and skeletal muscle, and low
 CC in testis. Also found in many cell lines, highest expression in
 CC cells of the immune system.
 CC -!- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
 CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
 CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
 CC AND VICE VERSA.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; UI3737; AAA65015.1; -;
 DR EMBL; UI3738; AAB60355.1; -;
 DR EMBL; U26943; AAA74929.1; -;
 DR EMBL; AJ413269; CAC88866.1; -;
 DR EMBL; AY219866; AAO25654.1; -;
 DR EMBL; BC016926; AAH16926.1; -;
 DR PIR; A55315; A55315;
 DR PDB; 1PAU; 07-JUL-97.
 DR PDB; 1CP3; 24-DEC-97.
 DR PDB; 1GFW; 23-JUN-00.
 DR MEROPS; C14.003; -;
 DR Genew; HGNC:1504; CASP3.
 DR MIM; 600636; -;
 DR GO; GO:0004208; F.caspase-3 activity; TAS.
 DR GO; GO:0008624; P.induction of apoptosis by extracellular sig. .; TAS.
 DR GO; GO:0008629; P.induction of apoptosis by intracellular sig. .; TAS.
 DR GO; GO:0009403; P.pathogenesis; TAS.
 DR InterPro; IPR002138; ICE p10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS02007; CASPASE_P10; 1.
 DR PROSITE; PS02008; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
 KW 3D-structure.
 FT PROPEP 1 9
 FT PROPEP 10 28
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.


```

DR EMBL; U49929; AAC52764.1; -
DR EMBL; D86352; BAA21727.1; -
DR EMBL; Y13086; CAA73528.1; -
DR EMBL; U19522; AAC53196.1; -
DR EMBL; BC038825; AAH38825.2; -
DR EMBL; U63720; RAD09504.1; -
DR PIR; JCS410; JCS410.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -
DR MGD; MGI:107739; Casp3.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT CONFLICT 17 17 E -> G (IN REF. 2).
FT CONFLICT 51 51 SRS -> ARN (IN REF. 6).
FT CONFLICT 63 65 SRS -> T (IN REF. 2).
FT CONFLICT 84 84 Q -> E (IN REF. 2).
FT CONFLICT 95 95 D -> E (IN REF. 2).
FT CONFLICT 97 97 L -> M (IN REF. 2).
FT CONFLICT 128 128 Y -> F (IN REF. 2).
FT CONFLICT 135 135 E -> D (IN REF. 2).
FT CONFLICT 231 231 E -> Q (IN REF. 6).
FT CONFLICT 262 262 I -> F (IN REF. 6).
SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;

Query Match 19.2%; Score 418; DB 1; Length 277;
Best Local Similarity 32.8%; Pred. No. 3.5e-28;
Matches 90; Conservative 50; Mismatches 92; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLIINNVNCRSGLTRGCSNIDCKELRRSSLLHFMVEVKGDLTA 209
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 DSSYKMDYEMGICIIINNKNEHKSGMSRSGTDVDAANLRETFMGLKYQVRNKNLDR 93
QY 210 KKMVLALLELARQDHGALDCVWVILSHGQCASHLQFPGAVYGTDCPVSVEKIVNIENG 269
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
94 EDILELMDSVSKEDHSKRSSFVCVILSHGDE-----GVYGTNG-FVELKKLTSFFRG 145
QY 270 TSCPSLGGKPKLFFTOACGEGEKDGHGFEVASTSPEDSGSNPEPDATPFQGLRTFDQL 329
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
146 DYCRLTGKPKLFIQACRGTELDGCIETDSDGTEDEM----- 182
QY 330 DAISLPTPSDFVSVPFGVSRVNRDPKSGSWYVETLDDIEQWAHSEDLQSLLRVAN 389
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
183 -ACQIPVEADFLYAYSTAPGYISWRNSKOGSWFIQSLGCSMLKLYAHKLEFMHILTRVN 241
QY 390 AVSVK-----GIYKMPGCFNFKLKKLF 413
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 KVATFESFSLDSTFHAKKQIPCIVSMLTKELYF 275

RESULT 6
ICE2_MOUSE
ID ICE2_MOUSE STANDARD; PRT; 435 AA.
AC P29594; O08737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 protein).

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GN OS CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated
RT expression in the mouse brain.";
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival. May be important in
CC multistep carcinogenesis.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- TISSUE SPECIFICITY: High level expression seen in the embryonic
CC CNS, liver, lung, kidney, small intestine, and hair follicles of
CC vibrissae. Moderate expression seen in the skin, oral mucosa,
CC skeletal muscle, submandibular gland and thymus. In the adult, it
CC is highly expressed in spleen, lung and kidney. Moderately in the
CC brain, heart, testis, liver. Low levels in the thymus, skeletal
CC muscle, ovary and gut.
CC -!- DEVELOPMENTAL STAGE: During embryonic development is highly
CC expressed in several types of mouse tissue undergoing high rates
CC of programmed cell death such as central nervous system and
CC kidney.
CC -!- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
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CC
CC EMBL; D28492; BAA25876.1; ALT_INIT.
CC EMBL; Y13085; CAA73527.1; ALT_INIT.
CC HSSP; P42574; 1CP3.
CC MEROPS; C14.006; -.
CC MGD; MGI:97295; Casp2.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00656; Peptidase_C14; 1.

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DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9 BY SIMILARITY.
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT CONFLICT 25 29 KSMDS -> QVD (IN REF. 4).
FT CONFLICT 170 170 C -> S (IN REF. 2).
FT CONFLICT 178 178 T -> A (IN REF. 2).
FT CONFLICT 182 182 M -> V (IN REF. 2).
FT CONFLICT 187 187 I -> K (IN REF. 2).
FT CONFLICT 190 190 E -> G (IN REF. 3).
FT CONFLICT 199 199 T -> S (IN REF. 2).
FT CONFLICT 211 211 D -> G (IN REF. 2).
FT CONFLICT 236 236 L -> I (IN REF. 4).
FT CONFLICT 245 245 T -> M (IN REF. 3).
SQ SEQUENCE 277 AA; 31491 MW; ADABRF418E2507402 CRC64;

Query Match 18.8%; Score 409; DB 1; Length 277;
Best Local Similarity 32.1%; Pred. No. 2e-27;
Matches 88; Conservative 52; Mismatches 92; Indels 42; Gaps 4;

QY 150 DLAYILMEPCGCHLIINNVCRESGLRTRTGSNIDCEKLRFRFSLFHFMVVGDLTA 209
Db 34 DSSYKMDYPMGLCIILNNKFNHFKTGMARSNGTDVDAANLRTFMALKYEVKNKDLTR 93
QY 210 KKMVLALLEARODHGALDCVVVILSHGQASHLOPPGAVYGTDCGPVSVEKIVNIFNG 269
Db 94 EEIMELMDSVSKEDHDKSRFSFVCIILSHGDE-----GVIFGTNG-PVDLKKLTSPFRG 145
QY 270 TSCPSLGGPKLFFIOACGGEQKHGFVASTSPEDSPCSNPEPATPFQGLRFTDQL 329
Db 146 DYCRLTGKPKFLIOACRGTELDGIEDTSGTDDM----- 182
QY 330 DAISLPTSDIFVSYSTFGFVSWDPKSGSVYETLDDIFEQWAHSDQLSLLLRVAN 389
Db 183 -ACQKIPVEADFLYAYSTAPGYYSWNSRDGWFQISLCAMLYAHKLEFHWHLTRVNR 241
QY 390 ANSVK-----GIYQMPGCFNFKLFF 413
Db 242 KVATEFESFLDTHFAKKQIPICVSMILTKELYF 275

RESULT 8
ICE2 HUMAN STANDARD; PRT; 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/18).
DE CASP2 OR ICH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
RL regulators of programmed cell death.";
RL Cell 78:739-750(1994).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
RP GLY-424.
```

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RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Doebber A., Martinka S., Maupin R.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shaham S., Horvitz H.R.;
RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine
RT protease with substrate specificities similar to those of the human
RT CPP32 protease.";
RT Genes Dev. 10:1073-1083(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ in the N- and C-termini;
CC Name=ICH-1L;
CC IsoId=P42575-1; Sequence=Displayed;
CC Name=ICH-1S;
CC Note=Acts as a positive regulator of apoptosis;
CC IsoId=P42575-2; Sequence=VSP_000801, VSP_000802;
CC Note=Acts as a negative regulator of apoptosis;
CC -!- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic
CC lung, liver and kidney than in the heart and brain. In the adults
CC higher level expression is seen in the placenta, lung, kidney,
CC pancreas than in the heart, brain, liver and skeletal muscle.
CC -!- PTM: THE MAJORE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
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CC -----
DR EMBL; U13021; AAA58959.1; -
DR EMBL; U13022; AAA58960.1; -
DR EMBL; AY219042; AAO25653.1; -
DR EMBL; AC073342; AAP22346.1; -
DR PIR; A54821; A54821.
DR HSP; P29466; IICB.
DR MEROPS; C14.006; -.
DR Genew; HGNC:1503; CASP2.
DR MIM; 600639; -.
DR GO; GO:0004202; F:caspase-2 activity; TAS.
DR GO; GO:0019899; F:enzyme binding; ISS.
DR GO; GO:0008633; F:apoptotic program; TAS.
DR GO; GO:0006508; F:proteolysis and peptidolysis; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
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```
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; thiol protease; Apoptosis; Zymogen; Polymorphism;
FT PROPEP 1 152
FT CHAIN 153 308
FT PROPEP 309 316
FT CHAIN 317 435
FT CHAIN 331 435
FT CHAIN 15 103
FT DOMAIN 260 260
FT ACT SITE 303 303
FT ACT SITE 303 303
FT VARSPLIC 1 14
FT VARSPLIC 306 435
FT VARSPLIC 155 155
FT VARIANT 161 161
FT VARIANT 424 424
FT MUTAGEN 303 303
FT MUTAGEN 352 352
FT SEQUENCE 435 AA; 48855 MW; 1652EC73F6286FB7 CRC64;
Query Match
Best Local Similarity 29.5%; Pred. No. 3.8e-27; Length 435;
Matches 127; Conservative 66; Mismatches 155; Indels 82; Gaps 13;
QY 9 LRRCLRLVEQLQDVLWLLSRLFRPHMIEDIQ-RAGSGRRDQARQLIIDEITRGS 67
Db 23 LKNRVVLAKQLLSLELLEHLEKDIITLRELIQAKVGSFS---QNVELLNLLPKRG 79
QY 68 QALPLFTSLCDETDQDMLASFLRN-----RQAGKL 98
Db 80 QAFDAFCALRETQGHLEDMLLTSLGLQHLVPLSCDYDLSPFPVCSCPLYKKLRL 139
QY 99 SKPTLENLT-----PVRLRPEIRKPEVLRPTPRPDVIGSGGFGDVGALSLRGADL 153
Db 140 STDIVHSLNDKQGVCLQ-----VKPCTP-----EFYQTHFQLAY 175
QY 154 ILSMEPCGHCUILNNVPCRSGLRTRGNSIDCEKLRFRSSSLHFMVEVKGDLTAKQW 213
Db 176 RLQSRPRGLALVLSNVHFTGKELEFRSGGVGDHSTLVTFLFKLLGYDVHVLCDQTAQEMQ 235
QY 214 LALLELAR-QDHGALDCCVVVLISHGQASHLQFPQAVVGTGDCPVSVKEIVNIFNGTSC 272
Db 236 EKLQNFALPARRVTVDSICVALLSHGVE-----GALYGVGDKLLQGVFQFQFDMNC 288
QY 273 PSLGKPKLFFIQAGGQKDHGEVASTSPEDSPGNSNPBPDPATPFQEGRLTFDQLDAI 332
Db 289 PSLQNKPKWFIQACRGDETDGVGDQDQKHNAGSPGCE-ESDA-----GREKLPKM--- 339
QY 333 SSLPTPSDIFVSYTFPGFVWRDPKSGSWVETLDDIFEQWAHSEDLOSLLLRVANAVS 392
Db 340 -RLPTRSDMIGYACLGKTAAMRNTRKGSWYIEALAQVFSEACDMHVMADMLVKV-NAL- 396
QY 393 VKGIYKQMPG 402
Db 397 INDEGYAPG 406
RESULT 9
ID CED3 CAEVU STANDARD; PRT; 496 AA.
AC P45436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3.
OS Caenorhabditis vulgariis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=31233;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94061982; PubMed=8242740;
RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
RT "The C. elegans cell death gene ced-3 encodes a protein similar to
RT mammalian interleukin-1 beta-converting enzyme.";
RL Cell 75:641-652(1993).
CC -!- FUNCTION: Acts as a cysteine protease in controlling programmed
CC cell death by proteolytically activating or inactivating a
CC substrate protein or proteins, a potential substrate may be ced-4.
CC Alternatively it might directly cause cell death by
CC proteolytically cleaving proteins that are crucial for cell
CC viability (By similarity).
CC -!- SUBUNIT: Could be a heterodimer of two subunits derived from the
CC precursor sequence by a probable autocatalytic mechanism.
CC -!- PTM: May be regulated by phosphorylation.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
DR HSPP; P42574; 1CP3.
DR MEROPS; C14.002; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; thiol protease; Zymogen; Apoptosis; Phosphorylation.
FT CHAIN 1 364
FT CHAIN 365 496
FT DOMAIN 1 91
FT ACT SITE 308 308
FT ACT SITE 351 351
FT SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;
Query Match
Best Local Similarity 18.7%; Score 407; DB 1; Length 496;
Matches 131; Conservative 74; Mismatches 159; Indels 170; Gaps 15;
QY 1 MDEADRR-LLRRCRLRLVEELQDVLWLLSRLFRPHMIEDIQRAGSG-----SRR 52
Db 1 MWRQDRRLLENTILVFNSKIQSEQLIDVLIAT-----DVLSNDGMDINSCTER 51
QY 53 DQARQLIIDEITRGSQALPLFISCLDPTGQDMLASFLR-----TNRQAGKLS 99
Db 52 DKRKEQKAVQRQGRDEAFRFDYDALRDTGHELLAAVLEPLATDLGCPSPASHRRSRLS 111
QY 100 KPTLENLTTPVVL-----RPEIRKPEVLRPET 125
Db 112 PPTSSPTFRVHRDSSVSSVSTSTVQDVYVTRASTSRSSRLPHTSDRHNYSVSPNSRPSQ 171
QY 126 PRPVDIGSGGFGDVGALSL-----LRGNADLAILSLME----- 158
Db 172 PSSANGSFTGCSLGYSSSRSTRSYSKASAHSCYIFHEEDMNYVDAPTHRVDEKTMVRN 231
QY 159 ---PCGHCLINNVNFCRESGLRTRTGSNIDCEKLRFRFSSILHFMVEVKGDLTAKKMLIA 215
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Db 232 FSTPRGLCLINNEHF---EQMPTNGTKADKONLWIFRCMGVTVICKONISGRGM-LT 287
Qy 216 LLELAROD-HGALDCCVVWILSHGQASHLQFPQAVGTGDCGVPVSKIVNIFNGTSCPS 274
Db 288 IRDFARNETHG--DSAILVILSHGEE-----NVIIIGVDVSVNVHIEVDLLNAANAPR 338
Qy 275 LGGPKLFFTOACGGEOKHGFEVASTSPEDSPGSGNPEPDATFPQGLRTFDOLDIAISS 334
Db 339 LANPKPLVFOACGERDNGFPV-----LDSVDGVPS 371
Qy 335 L-----PTPDSIFVSYTFPGFVSWRDPKSGSWVET 366
Db 372 LIRRGWDRDGNFLGCVRPQAOQWKKPSQADILIRYATAGYVWRNSARGSWFIQA 431
Qy 367 LDDIFEWAHSELDQSLLLRVANAVSV-----KGIYKQMGPCFNFLRKLJFF 413
Db 432 VCEVFSTHAKMDVDVLELLTEVKNKVCAGFQTSQGANILKQMPBMTSLLLKKFYF 485

RESULT 10
IC38_MOUSE
ID IC38_MOUSE STANDARD; PRT; 480 AA.
AC 089110; O35669;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-8 precursor (EC 3.4.22.-).
GN CASP8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=129/SVJ;
RX MEDLINE=98316661; PubMed=9654089;
RA Sakamaki K., Teukumo S.-I., Yonehara S.;
RT "Molecular cloning and characterization of mouse caspase-8.";
RL Eur. J. Biochem. 253:399-405(1998).
RN [2]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99057979; PubMed=9837723;
RA Van de Craen M., Van Loo G., Declercq W., Schotte P.,
RA Van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
RA Vandenabeele P.;
RT "Molecular cloning and identification of murine caspase-8.";
RL J. Mol. Biol. 284:1017-1026(1998).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
SEQUENCE OF 57-476 FROM N.A.
RP

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RA Kioschis P., Kischkel F., Poustka A., Kramer P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC Likely target for the coxsack virus CRVA death inhibitory protein.
CC -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
CC Interacts with Fadd, Cflar and Peal5 (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
CC Highest expression in spleen, thymus, lung, liver and kidney.
CC Lower expression in heart, brain, testis and skeletal muscle.
CC -!- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
CC day 7.
CC -!- TIM: Generation of the subunits requires association with the
CC death-inducing signaling complex (DISC), whereas additional
CC processing is likely due to the autocatalytic activity of the
CC activated protease. GZMB and CASP10 can be involved in these
CC processing events (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF067841; AAC40132.1; -
CC EMBL; AF067835; AAC40132.1; JOINED.
CC EMBL; AF067836; AAC40132.1; JOINED.
CC EMBL; AF067837; AAC40132.1; JOINED.
CC EMBL; AF067838; AAC40132.1; JOINED.
CC EMBL; AF067839; AAC40132.1; JOINED.
CC EMBL; AF067840; AAC40132.1; JOINED.
CC EMBL; AF067834; AAC40131.1; -
CC EMBL; AJ007749; CAA07677.1; -
CC EMBL; BC006737; AAH06737.1; -
CC EMBL; BC049955; AAH49955.1; -
CC EMBL; AJ000641; CAA04196.1; -
CC HSSP; Q15806; 1QDU.
CC MEROPS; C14.009; -
CC MGD; MGI:1261423; Casp8.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0004205; F:caspase-8 activity; IDA.
CC GO; GO:0006915; P:apoptosis; IDA.
CC InterPro; IPR001875; DED.
CC InterPro; IPR002138; ICE p10.
CC InterPro; IPR001309; ICE p20.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF01335; DED; 2.
CC Pfam; PF00656; Peptidase_C14; 1.
CC PRINTS; PR00376; ILIHCENZYME.
CC SMART; SM00031; DED; 2.
CC SMART; SM00031; DED; 2.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS02027; CASPASE_P10; 1.
CC PROSITE; PS02028; CASPASE_P20; 1.
CC PROSITE; PS0168; DED; 2.
CC Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat.
KW

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield F.S.N., Kryzyski M.I., Skalska U., Smalus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [10]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
RN [11]
RP FUNCTION.
RX MEDLINE=97160607; PubMed=9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956 (1997).
RN [12]
RP PROCESSING.
RX MEDLINE=97327557; PubMed=9184224;
RA Medema J.P., Scaffidi C., Kischkel P.C., Shevchenko A., Mann M.,
RA Krammer P.H., Peter M.E.;
RT "FLICE is activated by association with the CD95 death-inducing
RT signaling complex (DISC).";
RL EMBO J. 16:2794-2804 (1997).
RN [13]
RP CHARACTERIZATION OF ISOFORM 7.
RX MEDLINE=20318377; PubMed=10860845;
RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayashi K.;
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes.";
RL Biochem. Biophys. Res. Commun. 272:877-881 (2000).
RN [14]
RP INTERACTION WITH BCL2; BCL2L1 AND BCAP31.
RX MEDLINE=97477382; PubMed=9334338;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.;
RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
RT endoplasmic reticulum.";
RL J. Cell Biol. 139:327-338 (1997).
RN [15]
RP INTERACTION WITH PEAL5.
RX MEDLINE=99369240; PubMed=1042631;
RA Condorelli G., Vaghiotta G., Cafieri A., Trencia A., Andalo P.,
RA Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
RT "PED/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
RT induced apoptosis.";
RL Oncogene 18:4409-4415 (1999).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99451259; PubMed=10508784;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Gruetter M.G.;
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis.";
RL Structure 7:1125-1133 (1999).
RN [17]
RP VARIANT CASP8 TRP-248.
RX MEDLINE=22239940; PubMed=12353035;
RA Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Lenardo M.J.;
RT "Pleiotropic defects in lymphocyte activation caused by caspase-8
RT mutations lead to human immunodeficiency.";
RL Nature 419:395-399 (2002).
CC -!- FUNCTION: Most upstream protease of the activation cascade of

CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|AMC.
CC Likely target for the coxox virus CRMA death inhibitory protein.
CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
CC with the pro-apoptotic activity of the complex.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
CC endoplasmic reticulum with a complex containing BCAP31, BAF29,
CC BCL2 and/or BCL2L1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=9;
CC Name=1; Synonyms=Alpha-1;
CC IsoId=Q14790-1; Sequence=Displayed;
CC Name=2; Synonyms=Alpha-2, MCH5-beta;
CC IsoId=Q14790-2; Sequence=VSP_000810;

Query Match 17.6%; Score 383; DB 1; Length 479;
Best Local Similarity 25.2%; Pred. No. 7.2e-25;
Matches 122; Conservative 79; Mismatches 150; Indels 134; Gaps 17;
QY 5 DRLRLRRLRLVEELQVDQLVLLSRLPRHMIEDIQAGSGRRDQARQLIIDLET 64
DB 50 EKRMLESNLSFLKEL-----LFRINRL-DLLITYLNTKREMER---ELQT 92
QY 65 RGSQALPLFTICLEDQDMLASFLINR--QAQKLSKPTLE---NLTPVLRPEIR--- 116
DB 93 PGRAQISAYRVMLYQISEVSRSELRSFKILLQEEISKCKLDDMLLDIFIEMEKRVIL 152
QY 117 ---KPEVLR-----LNDYEFSEKSSLSLEGSDFESNGELGVMTISDSP 212
DB 153 GEGKLDILKRVCAQINKSLKLIINDYEFSEKSSLSLEGSDFESNGELGVMTISDSP 212
QY 127 RPVDIGSGFGDVGVALESRLGNADLAYLSMEPCGHCLIIINNVPFRE-----SGURT 179
DB 213 REQD-----SESQTLDKVYQMKSPRGYCLIIINNHFARAKREKVPKLHSIRD 259
QY 180 RTGSNIDCKLRPRFSSLHFMVVKGDLTAKM--VLALLEARQDHGALDCCVVVILSH 237
DB 260 RNGTHLDAGALTTFEELHFEIKPHDDCTVEQIVELIKYQL--MDHENMDCFICILSH 317
QY 238 GCQASHLQFPGAVYGTGCPVSVKEKIVNIFNGTSCPSLGGPKPLFFIACGGEQKDHGFE 297
DB 318 GDK-----GLIYGTGQEARPIVELTSQFTGLKCPSLAGPKVFFIACQGDNYQKGP 370
QY 298 VASTSPEDSPGSPNPEPDATPFQGLRFTFDQDAISS-----LPTPSDIFVSYSTPPGVS 353
DB 371 VETDSEEQ-----PYLE-----MDLSSPQTRVYPDEADFLGGMATVNNCVS 411
QY 354 WRDPKSGSWYVETL--DDIFEQWAHSEDLQSLI-----LVAANAVSVKGYKMGPCFNLR 408
DB 412 YRNFAEGWYIQSLCQSLRERCPRGDDILITLITVENVVSVNKKDKKNGKMQPQFTFLR 471
QY 409 KKLFF 413
DB 472 KKLVF 476

RESULT 13
ICE7 MESAU
ID ICE7 MESAU STANDARD; PRT; 303 AA.
AC P55214;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
DE (SCA-2).
GN CASP7 OR MCH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=SVRian; TISSUE=Liver;
RX MEDLINE=96224303; PubMed=8643593;
RA Pai J.-I., Brown M.S., Goldstein J.L.;
RT "Purification and cDNA cloning of a second apoptosis-related cysteine
RT protease that cleaves and activates sterol regulatory element binding
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC !- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC regulatory element binding proteins (SREBPs). Proteolytically
CC cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
CC bond. Overexpression promotes programmed cell death (By
CC similarity).
CC !- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
CC (By similarity).
CC !- SUBCELLULAR LOCATION: Cytoplasmic.
CC !- PTM: CLEAVAGES BY GRANTZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC !- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC -----
CC EMBL: U47332; AAC2595.1; -.
CC HSP: P42574; IPAU.
CC MEROPS: C14.004; -.
CC InterPro: IPR002138; ICE_p10.
CC InterPro: IPR001309; ICE_p20.
CC InterPro: IPR002398; Peptidase_C14.
CC Pfam: PF00656; Peptidase_C14; 1.
CC PRINTS: PR00376; IULBENZYM.
CC SMART: SM00115; CASc; 1.
CC PROSITE: PS01122; CASPASE_CYS; 1.
CC PROSITE: PS01121; CASPASE_HIS; 1.
CC PROSITE: PS0207; CASPASE_P10; 1.
CC PROSITE: PS0208; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match
Best Local Similarity 16.7%; Score 364.5; DB 1; Length 303;
Matches 92; Conservative 40; Mismatches 98; Indels 43; Gaps 7;

QY 153 YILMEFGHCLINNVCRESGLTRTGSGNIDCEKLRFRFSSLLHFVMEVKGDLTKKM 212
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
60 YRMDFKMGKCIINNKNFDKVTGMVRNGTDKDAALFKCFSLGFDVVVYNDSCAKM 119
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QY 213 VIALLELARQDHGALDCVVVILSHGQASHLQFPGAVYGTDCGCVSEKIVFNFTSC 272
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 QDLLRKASBEDHSNSACFACVLLSHGEE-----NLIYKGVG-TPIKDLTAHFRGDR 171
QY 273 PSLGKPKLFFIOACGGEQKDXHFEVASTSPESPGSNPEPDATPQEGRLTFDQDAI 332
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
172 KTLLEKPKLFFIOACRGTELDGQVADS-----GPINETDANPRYK----- 212
QY 333 SSLSPTSDIFVSSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQ--SLLLRVANA 390
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
213 --IPVEADELFAYSTVPGYYSWRNPGKSWFVALCSILDE--HGKDLFIMQLITRVNDR 268
QY 391 VS-----VKGYYKQMPGCFNFKLKLFF 413
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
269 VARHFSQCDDPCDFNEKKQIPCMVSMLTKEYLF 301

RESULT 14
ICE7_HUMAN
ID ICE7_HUMAN STANDARD; PRT; 303 AA.
AC P55210; Q13364; Q96BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).
GN CASP7 OR MCH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
RA Dixit V.M.;
RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
RT factor-induced apoptosis."
RL J. Biol. Chem. 271:1621-1625(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Spleen;
RX MEDLINE=96147144; PubMed=8567622;
RA Lippke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
RT cysteine protease similar to CPP32."
RL J. Biol. Chem. 271:1825-1828(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salveson G.,
RA Earnshaw W.C., Litwack G., Alnemri E.S.;
RT "Mch3, a novel human apoptotic cysteine protease highly related to
RT CPP32."
RL Cancer Res. 55:6045-6052(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
RC TISSUE=Fetal lung, and Fetal spleen;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genomics 40:86-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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QM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:20 ; Search time 17 Seconds
(without alignments)
2353.863 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRCRLRLVSEL.....YKMPGCFNLRKLLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	2 G02635	ICE-LAP6 - human
2	1658	76.1	454	2 JC7123	caspase-9 long cha
3	429	19.7	277	2 S64710	cysteine proteinas
4	418	19.2	277	2 A55315	cysteine proteinas
5	414	19.0	452	2 JC6507	caspase-2 - rat
6	409	18.8	435	2 A54821	apoptosis regulato
7	408	18.7	277	2 JC5410	CPP32 protein - mo
8	387.5	17.8	503	2 A49429	interleukin-1 beta
9	384	17.6	212	2 I67437	cysteine proteinas
10	362	16.6	495	2 T20038	hypothetical prote
11	304	13.9	312	2 B54821	apoptosis regulato
12	268.5	12.3	402	2 A64495	fl-1 beta converta
13	262	12.0	182	2 I67436	interleukin-1-beta
14	262	12.0	826	2 T43638	caspase-related pr
15	259	11.9	404	2 A42677	interleukin-1 beta
16	256.5	11.8	383	2 A56084	interleukin-1-beta
17	242.5	11.1	536	2 T43633	caspase-related pr
18	239.5	11.0	242	2 JC7517	caspase-14/a - hum
19	236	10.8	642	2 T27021	hypothetical prote
20	220	10.1	311	2 B56084	interleukin-1-beta
21	210	9.6	418	2 B57511	interleukin-1 beta
22	209	9.6	377	2 A57511	interleukin-1-beta
23	209	9.6	488	2 T13385	hypothetical prote
24	186	8.5	263	2 C56084	interleukin-1-beta
25	154.5	7.1	149	2 T43637	caspase protein 1C
26	151.5	6.9	136	2 I53300	interleukin-1-beta
27	115.5	5.3	394	2 T26968	hypothetical prote
28	108.5	5.0	589	2 T52070	RNA1 protein homol
29	107.5	4.9	139	2 T43642	caspase protein 3

30	106.5	4.9	589	2 A36983	RNA1 homolog fugl1
31	96.5	4.4	369	2 T32781	hypothetical prote
32	93.5	4.3	579	2 S46210	3-dehydroquinat d
33	92.5	4.2	4302	2 A38971	polycystic kidney
34	92	4.2	5327	2 T13564	microtubule-associ
35	91.5	4.2	376	2 JC7759	alcohol dehydrogen
36	91	4.2	808	2 A96791	hypothetical prote
37	89.5	4.1	395	2 T05906	probable polygalac
38	89	4.1	369	2 T20505	hypothetical prote
39	89	4.1	879	2 AC2347	hypothetical prote
40	88	4.0	629	2 T48799	Rp9p related prot
41	87.5	4.0	518	2 JC7387	testis-abundant fi
42	87.5	4.0	697	2 A86402	protein T2205.17 [
43	87	4.0	1221	2 A49457	fibulin-2 precursor
44	87	4.0	5762	2 A41819	proline-rich pepti
45	86.5	4.0	467	2 T02238	glucosyl transfera

ALIGNMENTS

RESULT 1
G02635
ICE-LAP6 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02635
R;Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
submitted to the EMBL Data Library, April 1996
A;Reference number: H01513
A;Accession: G02635
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-416 <DUA>
A;Cross-references: EMBL:U56390; NID:gl336026; PIDN:AAC50640.1; PID:gl336027

Query Match 100.0%; Score 2180; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. NO. 8.6e-179;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDEADRLRLRCRLRLVSELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII	60
Db	1	MDEADRLRLRCRLRLVSELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII	60
QY	61	DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGLSKPTLENLTPVLRPEIRKPEV	120
Db	61	DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGLSKPTLENLTPVLRPEIRKPEV	120
QY	121	LRPETPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLIIINNVMFCRESGLRTR	180
Db	121	LRPETPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLIIINNVMFCRESGLRTR	180
QY	181	TGSNIDCEKLRFRFSLHFMVSKGDLTAKKMWLALLEARODHGALDCCVVILSHGQQ	240
Db	181	TGSNIDCEKLRFRFSLHFMVSKGDLTAKKMWLALLEARODHGALDCCVVILSHGQQ	240
QY	241	ASHLOFPGAVYTDGCPVSVEKIVNIFNGTSCPSLGGPKLFFIOACGGEQKHGFEVAS	300
Db	241	ASHLOFPGAVYTDGCPVSVEKIVNIFNGTSCPSLGGPKLFFIOACGGEQKHGFEVAS	300
QY	301	TSPEDESGSNPEPDATPFQGLRTFDQLDAISSLTPTSDIFVSVSTTFPGFVSWRDKSG	360
Db	301	TSPEDESGSNPEPDATPFQGLRTFDQLDAISSLTPTSDIFVSVSTTFPGFVSWRDKSG	360
QY	361	SNWVETLDDIEQWAHSEDLQSLILRVANAVSVKGIYQKMPGCFNLRKLLFFKTS	416
Db	361	SNWVETLDDIEQWAHSEDLQSLILRVANAVSVKGIYQKMPGCFNLRKLLFFKTS	416

RESULT 2
JC7123
caspase-9 long chain - mouse
C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: JC7123
R;Fujita, E.; Jinbo, A.; Matsuaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A;Reference number: JC7123; MUID:20001956; PMID:10529400
A;Accession: JC7123
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 76.1%; Score 1658; DB 2; Length 454;
Best Local Similarity 72.5%; Pred. No. 5.1e-134;
Matches 329; Conservative 24; Mismatches 63; Indels 38; Gaps 2;

QY 1 MDEADRLRLRRCLRLVEELQVQDLWDVLLSRELFRPHMIEDIQAGSGRRRDOARQLII 60
DB 1 MDEADRLRLRRCLRLVEELQVQDLWDVLLSRELFRPHMIEDIQAGSGRRRDOARQLVT 60
QY 61 DLETRGQALPLFTISCLEDTGQDMLASFLTRNQAGKL----- 98
DB 61 DLETRGQALPLFTISCLEDTGQDMLASFLTRNQAGKL----- 98
QY 99 -----SKPTLENLFPVLRPE-----IRKPEVLRPETPRPVDIGSGFGDYGAL 142
DB 121 AKERQVVKLPSQAVGNLFPVVLGPBELWPARKPEVLRPETPRPVDIGSGGADVCVP 180
QY 143 ESLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFWVE 202
DB 181 GKIRGNADWAYLTDSPCGCHLIINNPNFCRESSGLRTRTGSNIDRDKLEHFRFLRWFVE 240
QY 203 VKGDLTAKKVVALLLELARDHGDCCVVVILSHGCOASHLQPPGAVYGTDCGCPVSVEK 262
DB 241 VKNDLTAKKVMVATLMEMAHNRHRLDCFFVVVILSHGCOASHLQPPGAVYGTDCGCVSIEK 300
QY 263 IVNIFNCTGSPSLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEG 322
DB 301 IVNIFNCTGSPSLGGKPKLFFIQACGGEQKHGFEVASTSQGRITLSDSEPDATPFQEG 360
QY 323 LRTPDQLDASSLTPSDIFVSYSTFPFGVSWRDPKSGVYVETLDDIFEOWAHSEDLQSL 382
DB 361 PRPLDQLDAVSSLTPSDILVSYSTFPFGVSWRDPKSGVYVETLDDIGLFLFOWARSED 420
QY 383 LLLRVANAVSKGYTKQMPGCFNLRKKLPKTS 416
DB 421 LLLRVANAVSKGYTKQIPGCFNLRKKLPKTS 454

RESULT 3
S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C;Species: Crictetus griseus (Chinese hamster)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S64710; S72395
R;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
A;Reference number: S64710; MUID:9618185; PMID:8605870
A;Accession: S64710
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-277 <WAN>
A;Cross-references: EMBL:U27463
R;Wang, X.
submitted to the EMBL Data Library, May 1995
A;Reference number: S72395
A;Accession: S72395
A;Molecule type: mRNA
A;Residues: 1-79, 'A', 81-146, 'Y', 148-277 <WAW>
A;Cross-references: EMBL:U27463; NID:gl244443; PIDN:AA01511.1; PID:gl244444
C;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 19.7%; Score 429; DB 2; Length 277;
Best Local Similarity 33.2%; Pred. No. 5.1e-29;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFWVEVKGLDTA 209
DB 34 DSSYKMDYPBMGVCIINNNKFNHFKSTGMTPRSGTDVDAAKLRFTFMNLKYEVRNKNLTLR 93
QY 210 KKMVLALLELARDHGDCCVVVILSHGCOASHLQPPGAVYGTDCGCPVSVEKIVNIFNG 269
DB 94 EEIVELMKNASKEDHRSKRSFVCVILSHGDE-----GVIFGTDG-PIDLKLTSTYFRG 145
QY 270 TSCPSLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQL 329
DB 146 DRCSLIGKPKLFFIQACRGTELDGCIETDSTGTEDDMT----- 183
QY 330 DATSSLTPSDIFVSYSTFPFGVSWRDPKSGVYVETLDDIFEOWAHSEDLQSLLLRVAN 389
DB 184 --CQKIPVEADFLYAYSTAFGYYSWRNPKDGSFQISLCSMLKLYAHKLEFMMHILTVNR 241
QY 390 AVSVK-----GIYKMPGCFNLRKKLPF 413
DB 242 KVATEFESPLDSTFFHAKKQIPCVSMLTKEYL 275

RESULT 4

A55315
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
N;Alternate names: cysteine proteinase CPP32
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C;Accession: A55315; S58899; I39005
R;Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
A;Reference number: A55315; MUID:95074098; PMID:7983002
A;Accession: A55315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-277 <FER>
A;Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666
R;Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant,
Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A;Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalia
A;Reference number: S58899; MUID:95319529; PMID:7596430
A;Accession: S58899
A;Molecule type: protein
A;Residues: 29-467176-189, 'E', 191-193 <NIC>
R;Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier
Cell 81, 801-809, 1995
A;Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
A;Reference number: A56924; MUID:95292347; PMID:7774019
A;Accession: I39005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-189, 'E', 191-277 <RES>
A;Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 19.2%; Score 418; DB 2; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.5e-28;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFWVEVKGLDTA 209
DB 34 DSSYKMDYPBMGVCIINNNKFNHFKSTGMTPRSGTDVDAAKLRFTFMNLKYEVRNKNLTLR 93
QY 210 KKMVLALLELARDHGDCCVVVILSHGCOASHLQPPGAVYGTDCGCPVSVEKIVNIFNG 269
DB 94 EEIVELMKNASKEDHRSKRSFVCVILSHGDE-----GIIFGTNG-PVDLKKLTNFRFG 145
QY 270 TSCPSLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQL 329

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Db      146 DRCSLTGKPKLFIQACRGTELDGCIETSGVDDM----- 182
QY      330 DAISSLTPSDIFVSYTTFPGFVSWRDPKSGSWYVETLDDIFEQAHSEDLQSLLLRVAN 389
Db      183 -ACHKIPVDADFLAYSTAPGYYSWRNSKGSWFIQSLCAMLKQYAKLEFMHLLTRVNR 241
QY      390 AVSVK-----GTYKMPGCFNLRKKLFF 413
Db      242 KVATEFESFSDATFHAKKQIPICVSMLTKELYF 275

RESULT 5
JC6507
caspase-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC6507
R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
A:Title: Cloning and expression of the cDNA encoding rat caspase-2.
A:Reference number: JC6507; MUID:98087427; PMID:9427555
A:Accession: JC6507
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <SAT>
A:Cross-references: GB:U77933; NID:g2769705; PTID:AAB96379.1; PID:g2769706

Query Match      19.0%; Score 414; DB 2; Length 452;
Best Local Similarity 28.5%; Pred. No. 1.9e-27;
Matches 125; Conservative 65; Mismatches 154; Indels 94; Gaps 12;

QY      4  ADPR-----LLRCRLRLVEELQDQVLDVLLSRELFRPHMIEDIQRAGS 48
Db      20 ADRRSRLAVCGMHPHQETLKKNRVVLAKQLLLSELLEKDIITLEMRELIIQ-AK 77
QY      49 GSRDQARQLIIDLETRGSGALPLFISCLDTGQDMLASFLRTN----- 92
Db      78 GGSFSONVELLNLPKRGQAQDAFCEALRETRKQGHLEDLTLTSLDIOHILPLSCDYD 137
QY      93 -----RQAGKLSKPTLENLT-----PVVLRPEIRKPEVLRPETERPVDPVIGSG 134
Db      138 SSLPFSVCBSPPHKQSRSLSTDTMEHSLDNGDGPCLQ-----VKPCTP----- 181
QY      135 GFGDVGALESRLGNADLAILSNPECGHCLINNVPFCRESGLRTRTGSNIDCEKLRRRF 194
Db      182 -----EFYQAHYQLAYRLOSQPRGLALVMSNVHFTGEKDLFRSGDGVDTTLVTLF 233
QY      195 SSLHFMVEVKGDLTAKKMWLALLELAR-QDHGALDCCVVVILSHGCGQASHLQFPGAVYGT 253
Db      234 KLLGYNVHLYDQTAGEQMEKLNQAFALPAHRVTDSCIVALLSHGVE-----GGIYGV 286
QY      254 DGCPSVEKIVNIENGTCSPSLGGPKLFFIQACGGEQKDHGFEVASTSPEDSPGNSPE 313
Db      287 DGKLLQLQVFRLEFNANCPSLQNKPMFFIQACRGDETRDGVQDQDQGNHQAQSPGCE-E 345
QY      314 PDATPFOEGLRTFDQLDAISSLPDSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQ 373
Db      346 SDAG--KESLMK-----RLPTRSDMTCGVACLGNAAMNTRKGSWYIEALQVFESE 396
QY      374 WAHSEDLQSLLLRVANAV 391
Db      397 RACDMHVDMLVKV-NAL 413

RESULT 6
A54821
apoptosis regulator ICH-1, stimulatory form L - human
C:Species: Homo sapiens (nan)
C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: A54821
R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994

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A:Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
A:Reference number: A54821; MUID:94373811; PMID:8087842
A:Accession: A54821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-435 <WAN>
A:Cross-references: GB:U13021; NID:g537291; PID:g537292
C:Keywords: alternative splicing; apoptosis

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Query Match      18.8%; Score 409; DB 2; Length 435;
Best Local Similarity 29.5%; Pred. No. 4.9e-27;
Matches 127; Conservative 66; Mismatches 155; Indels 82; Gaps 13;

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QY      9  LRRCRLRLVEELQDQVLDVLLSRELFRPHMIEDIQ-RAGSGRRQARQALIIDLETRGS 67
Db      23 LKKNRVVLAKQLLSLELLEKDIITLEMRELIIQAKVGSFS--QNVLLMLLPKRG 79
QY      68 QALPLFISCLDTGQDMLASFLRTN-----RQAGKL 98
Db      80 QAFDAFCEALRETRKQGHLEDMLLTLTSLGLQHVLPPLSCDYDLSLPFPVCBSCPLYKKLRL 139
QY      99 SKPTLENLT-----PVVLRPEIRKPEVLRPETERPVDPVIGSGFGDVGALESRLGNADLAY 153
Db      140 STDVSHSLDNKDGPPCLQ-----VKPCTP-----EFYQTHFQLAY 175
QY      154 ILSMEPCGHCLIIINNVPFCRESGLRTRTGSNIDCEKLRRRFSIHFWMVEVKGDLTAKKMW 213
Db      176 RLQSRPRGLALVLSNVHFTGEKLEFRSGDGVDSHTLVTLFKLLGVDVHVLCDTQAEQ 235
QY      214 LALLELAR-QDHGALDCCVVVILSHGCGQASHLQFPGAVYGTDCPCVSEKIVNIFNGTSC 272
Db      236 EKIQNPAQLPAHRVTDSCIVALLSHGVE-----CAIYVDGKLLQLQEVFQLEDNANC 288
QY      273 PSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDSPGNSPEPDATPFOEGLRTFDQLDAI 332
Db      289 PSLQNKPMFFIQACGDETRDGVQDQDQGNHQAQSPGCE-ESDA-----GKEKLPMK--- 339
QY      333 SSLPDSDFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQAHSEDLQSLLLRVANAVS 392
Db      340 -RLPTRSDMTCGVACLGNAAMNTRKGSWYIEALQVSEACDMHVDMLVKV-NAL- 396
QY      393 VKGIYKQMEG 402
Db      397 IKDREGYAFG 406

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RESULT 7

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JC5410
CPP32 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C:Accession: JC5410
R:Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
Biochem. Biophys. Res. Commun. 231, 770-774, 1997
A:Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
A:Reference number: JC5410; MUID:97224429; PMID:9070890
A:Accession: JC5410
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-277 <MUK>
A:Cross-references: DDBJ:D86352
A:Experimental source: embryo
C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

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Query Match      18.7%; Score 408; DB 2; Length 277;
Best Local Similarity 32.1%; Pred. No. 3.2e-27;
Matches 88; Conservative 52; Mismatches 92; Indels 42; Gaps 4;

QY      150 DLAYILSMEPCGHCLIIINNVPFCRESGLRTRTGSNIDCEKLRRRFSIHFWMVEVKGDLTA 209
Db      34 DSSYKMDYPENGICIIITNKFHKSTGMSSRGDIDVDAANRETFMGLKYEVNRKNDLTR 93
QY      210 KMWLALLELARQDHGALDCCVVILSHGCGQASHLQFPGAVYGTDCPCVSEKIVNIFNG 269

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Db 94 EIMELMDSVSKEDHKSRSFVCLVSHGDE-----GVIFGTNG-FVDLKKLTSEFRG 145
QY 270 TSCPSLGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQL 329
Db 146 DYCRLTGKPKLFIQACRGTELDGLETDSGTDEE----- 182
QY 330 DAISLPTPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWASEDLQSLLRVA 389
Db 183 -ACQKIPVADFLYATAPGYYSWRNSKDGSWFIQSLCSMLKLYAHKLEFMIHLTVNR 241
QY 390 AVSVK-----GIYKQMPGCFNLRKKLFF 413
Db 242 KVATEFESLDSTFHAKKQIPCIVSMITRELYF 275

RESULT 8
A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: A49429; T37312
R;Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A;Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int
A;Reference number: A49429; MUID:94061982; PMID:8242740
A;Accession: A49429
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <YU>
A;Cross-references: GB:L29052; NID:G6503232; PIDN:AAA27982.2; PID:G6503233
A;Note: sequence extracted from NCBI backbone (NCBI:139825, NCBI:P:139826)
A;Accession: T37312
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-417, 'R', 419-503 <YU>
A;Cross-references: EMBL:L29052; PIDN:AAA27982.1
C;Genetics:
A;Gene: ced-3
A;Introns: 45/3; 94/2; 179/3; 289/3; 361/1; 403/3; 483/3

Query Match 17.8%; Score 387.5; DB 2; Length 503;
Best Local Similarity 25.0%; Pred. No. 4.1e-25;
Matches 128; Conservative 79; Mismatches 188; Indels 117; Gaps 17;

QY 1 MDEADRR-LLRRCRLRLVEELQVDLWDLVLSLRFPHMTEDIQAGSGRRQARQLI 59
Db 1 MWRQDRRLRNIMWFSSHLKVDLELLEVLIAQVLSNDGMDIN--SCGTVREKRREIV 58
QY 60 IDLETRGSOALPLFISCLEDTQDMIASFLR-----TNRQAGKLS 99
Db 59 KAVQRGDAVAFDAFYDALRSTGHEGLAEVLPLARSVDNSNAVEFECMPSAHRSRALS 118
QY 100 -----KPT-----LENLTPVVLRLPEIRK-----PEVLRPPTP 126
Db 119 PAGYSPTRVHRDSVSSVSTSTQDIYSRARSRSRSLHSDRHNSYSPVNAFFSQP 178
QY 127 RPVDIGSGGFGVGVGALES-----LRGNADLAYILSME----- 158
Db 179 SSANSSFTGCSLGYSSSRNRSFSKASGTQYIFHEEDNFVDAPTISRVFDEKTYERNF 238
QY 159 --PCHCLITINNPNFCRESGLRTRGSDNIDCEKLRFRFSSLHEMVVEVKGDLTAKMWLAL 216
Db 239 SSPRGWCLIIINHEF---EQMPTNRGTAKDNLTNLFRCMGYTVCKDNLTGRGLITI 295
QY 217 LELAR-QDHGALDCCVWLISHGCOASHLPFGVYGTGCPVSVKEIKVINFGTSCPSL 275
Db 296 RDAKHESHG--DSAILVLSHGEE-----NVLIGVDDIPISHTIYDLNNAAPRL 346
QY 276 GKPKLFTIQACGGKQKHGFVASTSPEDSRG-----SNPEPDATPFQEGRLTFDQL 329
Db 347 ANKPKIVFVQACKGERRDNGFFVLDS--VDGVPAFLRRGWRNDRDGLFNFLGCVR--FQV 402

QY 330 DAI-SSLPTPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWASEDLQSLLRVA 388
Db 403 QQVWRKKPSQADLLIAYATTAQVSVNRNSARGSWFCAVCEVSTHAKOMDVVELLTVN 462
QY 389 NAVSV-----KGIYKQMPGCFNLRKKLFF 413
Db 463 KKVACGFQTSQGSNILKQMPDMSRLKKFYF 494

RESULT 9
I67437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I67437
R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirschfield, A.N.; T
Endocrinology 136, 5042-5053, 1995
A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian ce
nuloza cells of the ovarian follicle.
A;Reference number: I53300; MUID:96042508; PMID:7588240
A;Accession: I67437
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <RES>
A;Cross-references: EMBL:U34685; NID:g1004370; PIDN:AA52261.1; PID:g1004371
C;Keywords: cysteine proteinase; hydrolase

Query Match 17.6%; Score 384; DB 2; Length 212;
Best Local Similarity 33.2%; Pred. No. 2.5e-25;
Matches 79; Conservative 46; Mismatches 81; Indels 32; Gaps 3;

QY 150 DLAVLSMEPCGHCILINNPNFCRESGLRTRGSDNIDCEKLRFRFSSLHFMVEVKGDLTA 209
Db 5 DSSYMDYPDWGLCIIINNPNFKHSTGMSARNGTDVAANLRFTFMALKYEVNRKNDLTR 64
QY 210 KQVIALLELARQDHGALDCCVWLISHGCOASHLPFGVYGTGCPVSVKEIKVINFG 269
Db 65 BEIMELMDSVSKEDHKSRSFVCLVSHGDE-----GVIFGTNG-FVDLKKLTSEFRG 116
QY 270 TSCPSLGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQL 329
Db 117 DYCRLTGKPKLFIQACRGTELDGLETDSGTDEE----- 153
QY 330 DAISLPTPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWASEDLQSLLRV 387
Db 154 -ACQKIPVADFLYATAPGYYSWRNSRSGSWFIQSLCMLKLYAHKLEFMIHLTV 210

RESULT 10
T20038
hypothetical protein C48D1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20038
R;Burton, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19214
A;Accession: T20038
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-495 <WIL>
A;Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
C;Genetics:
A;Gene: CESP:C48D1.2
A;Map position: 4
A;Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 16.6%; Score 362; DB 2; Length 495;
Best Local Similarity 24.6%; Pred. No. 6.2e-23;
Matches 118; Conservative 77; Mismatches 175; Indels 110; Gaps 16;

QY 5 DRR-LLRRCRLRLVEELQVDLWDLVLSLRFPHMTEDIQAGSGRRQARQLIIDLE 63

```
Db 4 DRSLLERNIMPSHLKVDLEILVIAKQVLSNDGDMIN--SCGVREKRREIVKAVQ 61
QY 64 TRGSQALPLFISCLEDTGQDMLASFTR-----TNRAQKLS----- 99
Db 62 RRGDVAFDAFYDALRSTGHEGLAEVLEPLARSVDNSNAVEFCPMPSPASHRSRALSAGY 121
QY 100 -KPT-----LENLTPVVLREIRK-----PEVLRPETRPVVD 130
Db 122 TSRTVRHDSVSVSFTSYQDIYSRARSRSRALHSSDRHNSPVPVNAFSPQSSAN 181
QY 131 IGSFGFGDVGALES-----LRGNADLAYILSME-----PC 160
Db 182 SSTFGCSLGYSSRRNSFSKASGPTQYIFHEDMFVDAPTISRVDKMTWRNFSPPR 241
QY 161 GHCLIIINVNFRESGLRTRTGNIDCEKLRFRFSSLHFVVEKGDITAKKMLLALLELA 220
Db 242 GMCLIIINNEHF---EQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRDA 298
QY 221 R-QDHGALDCCVVVILSHGCOASHLOFPFGAVYGTGDCPVSVEKIVNFNGTSCPSLGGKP 279
Db 299 KHESHG--DSAILVILSHGEE-----NVIIIGVDIPITSTHEIYDLLNAANAPRLANKP 349
QY 280 KLFFIQACGGEQKHGFVEASTSPEDSPG-----SNPEPDATPFOEGLRTEFDQDAI- 332
Db 350 KIVFVQACGERRDNGFPVLDS--VDCVPAFLRGRWDRDGPFLNFGCVR--PQVQVW 405
QY 333 SSLPTSDIFVSYSTPFGFVSWRDPKSGVSVETLDDIFEQWAHSEDLQSLLRVANAYS 392
Db 406 RKKPSQADILIAVATTAAQYVSWRNSARGSWFIQAVCEVFTSHAKDMVDVVELLTVKNKVA 465

RESULT 11
B54821
apoptosis regulator ICH-1, suppressive form S - human
C:Species: Homo sapiens (man)
C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54821
R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A:Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
A:Reference number: A54821; MUID:94373811; PMID:8087842
A:Accession: B54821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-312 <WAN>
A:Cross-references: GB:U0322
C:Keywords: alternative splicing; apoptosis

Query Match 13.9%; Score 304; DB 2; Length 312;
Best Local Similarity 29.7%; Pred. No. 3.1e-18;
Matches 94; Conservative 48; Mismatches 105; Indels 70; Gaps 8;

QY 9 LRRCRLRVVEELQVQDMLVLSRELFPRPHMIEDIQ-RAGSGRRDQARQLIIDLETRGS 67
Db 9 LKKNRWLAKQLLSLELLEKIOITLEMBELQAKVGSFS---QNVLLNLNLPKRG 65
QY 68 QALPLFISCLEDTGQDMLASFRTN-----RQAGKL 98
Db 66 QAFDAFCEALRETQCHLEDMLTLTSLGHLQHVLPPLSCDYDLSLPFFVCESPLYKCLR 125
QY 99 SKPTLENLT-----PVVLRPEIRKPEVLRPETRPVVDIGSGFGDVGALESIRGNADLAY 153
Db 126 STDTHVSLNDKDGVPCLQ-----VKPCTP-----EFYQTHFQLAY 161
QY 154 ILSMPCGCHLIINNPNFCRESGLRTRTGNIDCEKLRFRFSSLHFVVEKGDITAKKMW 213
Db 162 RLQSRPRGLAVLSNVHFTGKELBFRSGVDHSLTLVLFKLGVDVHVLCDQTAQEMQ 221
QY 214 LALLELAR--QDHGALDCCVVVILSHGCOASHLOFPFGAVYGTGDCPVSVEKIVNFNGTSC 272
Db 222 EKLQWFAQLPAHRVTDSCIVALLSHGVE-----GAIYGVGDKLLQLQEVFQLFDNANC 274
```

```
QY 273 PSIGGPKPKLFFIQACGG 289
Db 275 PSIQNKPKMFFIQACRG 291
```

RESULT 12

A46495

IL-1 beta convertase - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A46495; A47258; I48911

R:Wett, M.A.; Cerretti, D.P.; Berson, D.R.; Seavitt, J.; Gilbert, D.J.; Jenkins, N.A.; C

J. Immunol. 149, 3254-3259, 1992

A:Title: Molecular cloning of the murine IL-1 beta converting enzyme cDNA.

A:Reference number: A46495; MUID:93056487; PMID:1431103

A:Accession: A46495

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-402 <NET>

A:Cross-references: GB:I03799; NID:G198379; PIDN:AAA39306.1; PID:G198380

A>Note: sequence extracted from NCBI backbone (NCBIP:117473)

R:Mollineux, S.M.; Casano, F.J.; Rolando, A.M.; Peterson, E.P.; Limjuco, G.; Chin, J.; C

ard, A.D.; Thornberry, N.A.; Kostura, M.J.

proc. Natl. Acad. Sci. U.S.A. 90, 1809-1813, 1993

A:Title: Interleukin 1 beta (IL-1 beta) processing in murine macrophages requires a stru

A:Reference number: A47258; MUID:93189587; PMID:8446594

A:Accession: A47258

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-187,189-402 <MOL>

A:Experimental source: macrophage

A>Note: sequence extracted from NCBI backbone (NCBIP:126931)

R:Casano, F.J.; Rolando, A.M.; Mudgett, J.S.; Mollineux, S.M.

Genomics 20, 474-481, 1994

A:Title: The structure and complete nucleotide sequence of the murine gene encoding inte

A:Reference number: A54264; MUID:94307735; PMID:8034321

A:Accession: I48911

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 'MAV', 7-402 <RES>

A:Cross-references: EMBL:U04269; NID:G476217; PIDN:AAA56992.1; PID:G476218

C:Genetics:

C:Introns: 6/1; 92/1; 113/1; 150/3; 208/3; 287/1; 334/1; 370/3

Query Match

Best Local Similarity 24.7%; Pred. No. 4.8e-15;

Matches 110; Conservative 62; Mismatches 183; Indels 91; Gaps 16;

```
QY 7 RLRRCLRLVVEELQ---VDQLMDVLLSRELFPRPHMIEDIQ-RAGSGRRDQARQLIIDLE 63
Db 4 KILRAKQKQFINSVSTIGTINGLLLEKRVLNQEMDKIKLANI-TAMDKARDLCDHVS 62
QY 64 TRGSQALPLFIS---CLEDTGQDMLASF-----RTN 92
Db 63 KAGPQASQIFITYICNEDC---YLAGILELOSAPSAETVATEDSKGHPSSSETKEON 119
QY 93 RQAGKLSKPTLENLTPVVLREIRKPEVLRPETRPVVDIGSGFGDVGALESIRGNADLAY 152
Db 120 KEDG-----TPGLTGTCLKFCPLKAKLWKENP-----SEIYPIIMNTTRTRUA 164
QY 153 YILSMPCGCHLIINNPNFCRESGLRTRTGNIDCEKLRFRFSSLHFVVEKGDITAKKM 212
Db 165 -----LIICNTEF---QHLSPRVGAQVDLREMKLLLEDLGYTVKVNENLTALEM 210
QY 213 VLALLELAR--QDHGALDCCVVVILSHGCOASHLOFPFGAVYGTGDCPV-SVEKIVNFNGT 270
Db 211 VKEVKEFAACPEKTKTSDTFLVFMHSGIQEG---ICGTTYSNEVSDILKVDITFQMNTL 267
QY 271 SCPSLGGKPKLFFIQACGGEQKHGFVEASTSPEDSPGSGNPEPDATPFOEGLRT---PD 327
Db 268 KCPSLKDKPKVLIQACGGEKQ--GVULLKDSVRDS-----EEDFLTDAIFE 312
QY 328 QLDAISSLPTSDIFVSYSTPFGFVSWRDPKSGSVYVETLDDIFEQWAHSEDLQSLLRV 387
```

Db 313 D-DGIIKAHTEKDFIAFCSTPDNVSWRHVPVRSGLFIESLIKHMKEVAMSCDLEDIFPKV 371
QY 388 ANAVSVKGIYKQMPGCFNFKLFF 413
Db 372 RFSPEQPEPRLQMTADRVLTTRKFY 397

RESULT 13
I67436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I67436
R;Flaws, J.A.; Kugu, K.; Tbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Til
Endocrinology 136, 5042-5053, 1995
A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
lulosa cells of the ovarian follicle.
A;Reference number: I53300; MUID:96042508; PMID:7588240
A;Accession: I67436
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-182 <RES>
A;Cross-references: EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g1004369

Query Match 12.0%; Score 262; DB 2; Length 182;
Best Local Similarity 33.3%; Pred. No. 5.9e-15;
Matches 63; Conservative 33; Mismatches 75; Indels 18; Gaps 4;

QY 159 PCGHCLINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHFMVVKGLDTAKKVLALLE 218
Db 1 PRGLALVNSVHFTGEKDLFRSGDGVHTLTLVLFKLLGVNVHVLVDQTAQENQEKLN 60
QY 219 LAR-QDHGALDCCVWVILSHGCGQASHLQFPGAVYGTDCPVSVSEKIVNINFGTSCPSLGG 277
Db 61 FAQLPAHRVTDSCIVALLSHGVE-----GGIYGVGDKLLQLQEVRLFDNANCPSLQN 113
QY 278 KPKLFFTOACGGEQKDHGFVASTSPDESPGSPNPDPAFPQGLRTFDOLDIAISLPT 337
Db 114 KPRMFFTOACGGEQKDHGFVASTSPDESPGSPNPDPAFPQGLRTFDOLDIAISLPT 337
QY 338 PSDIFVSYS 346
Db 164 RSDMICVYA 172

RESULT 14
T43638
caspase-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans
N;Contains: caspase 2B
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43638; T43639
R;Shaham, S.
J. Biol. Chem. 273, 35109-35117, 1998
A;Title: Identification of multiple Caenorhabditis elegans caspases and their potential
A;Reference number: 222587; MUID:99074291; PMID:9857046
A;Accession: T43638
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-826 <SHA>
A;Cross-references: EMBL:AF088288; NID:g4063373; PIDN:AAC98295.1; PID:g4063374
A;Accession: T43639
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 564-826 <SH2>
A;Cross-references: EMBL:AF088289; NID:g4063375; PIDN:AAC98296.1; PID:g4063376
C;Genetics:
A;Gene: csp-2
A;Map position: 4
C;Keywords: cysteine proteinase; hydrolase

Query Match 12.0%; Score 262; DB 2; Length 826;

Best Local Similarity 23.8%; Pred. No. 4.6e-14;
Matches 96; Conservative 57; Mismatches 142; Indels 108; Gaps 12;
QY 86 ASFLRNROAGKUSKLTLENLTPVLRPEIRKEVLRPETPRVDIG----- 132
Db 455 AALEQSQNEQSNSTDDAVESDDVPAPQ-----SPPTSPADFGFTTSSSLTQDPA 507
QY 133 --SGFGDYGALES-----RGNADLAVILSMPCGH----- 162
Db 508 SNATGFSVPAPOAPPTSPADGPTTSSSLTQDPASNATGSGSPSPNSFETRMNCE 567
QY 163 -----CLINNVNFCRESGLRTRTGSNIDCEKLRFRFSLH 199
Db 568 DASDGKKIDETRYNNRNSKCAIINNVPFC--GMEXKRGSDKKKSLKFLERLGY 624
QY 200 MVEVKGDLTAKKMWLALLEARQDHGALDCVWVILSHGCGQASHLQFPGAVYGTDCGVS 259
Db 625 QSTSYDNLSKSEILETVRQFTQSNHG--DSLITIMSHGQD-----GLLYGVGVFPVQ 675
QY 260 VEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFVASTSPS--DESPGSPNPDPA 317
Db 676 MLDLIIDLM-----CTASLAKKPKWLMCVCCGRIDRAVRCDFIDNFDREPXF----- 725
QY 318 PFOEGLRTFDQLDAISLPTSPSIFVSYSFTPGFVSWRDPKSGSWYVETLDDIPEQWAS 377
Db 726 -FQPMKSKPPSHOTSSS---QADLLVSFSTSPGFLSPRDETGTGTWYIQELYRVIIENAKD 781
QY 378 EDIQLSLLLRVANAV-----SVKGIYKQMPGCFNFKLFF 413
Db 782 TLHADLLMETNRRVVEKYEADKVIVCKQAPFWSRFTKQLFF 824

RESULT 15
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: A54263; A42677; S21734; S24164
R;Carretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; S
Genomics 20, 468-473, 1994
A;Title: Molecular characterization of the gene for human interleukin-1beta converting
A;Reference number: A54263; MUID:94307734; PMID:8034320
A;Accession: A54263
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-404 <CR2>
A;Cross-references: GB:I27475
R;Carretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T. T
Science 256, 97-100, 1992
A;Title: Molecular cloning of the interleukin-1beta converting enzyme.
A;Reference number: A42677; MUID:92229430; PMID:1373520
A;Accession: A42677
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-404 <CER>
A;Cross-references: GB:M87507; NID:g435598; PIDN:AAA6942.1; PID:g186286
R;Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M
J.; Ding, G.J.P.; Egger, L.A.; Gaffney, E.P.; Lamjucio, G.; Palyha, O.C.; Raju, S.M.; Ro
cci, M.J.
Nature 356, 768-774, 1992
A;Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proc
A;Reference number: S21734; MUID:92244338; PMID:1574116
A;Accession: S21734
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-404 <THO>
A;Cross-references: EMBL:X65019; NID:g33792; PIDN:CAA46153.1; PID:g33793
R;Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992
A;Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
A;Reference number: S24164; MUID:92337439; PMID:1321594
A;Accession: S24164
A;Status: preliminary

A:Molecule type: protein
A:Residues: 120-135,'AX',138-139,'X',141-142 <KRO>

C:Genetics:
A:Gene: GDB:ILLBC

A:Cross-references: GDB:132368; OMIM:147678

A:Map position: 11q23-11q23

C:Keywords: cysteine proteinase; hydrolase

```
Query Match          11.9%; Score 259; DB 2; Length 404;
Best Local Similarity 24.3%; Pred. No. 3.1e-14;
Matches 104; Conservative 62; Mismatches 176; Indels 86; Gaps 14;

QY 10 RRCLRLVELOVDLWLLSKELFRPHMIEDIORAGSGSRDQARQLIIDLETGSOA 69
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 RKLFRSMGEGINGLLDELQTRVLNKEEMEKVRE-NATVMDKTRALIDSVIPKGA 68
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 70 LPLFIS--CLED-----TCQDMLASFRLTRNQAGKLSKPTLENTPVVLRPEIRK 118
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 CQICITYICEEDSYLAGTLGLSADQTSNYLNMQDSQGVLS-----SFPAP 114
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 119 EVLRPETRPVDIGSGGFDVGALLESL-----RGNADLAYILSMBPCHG-CLII 172
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 QAVQDNPAIPTSGSGEGNVKLSLEEAQRIWKQSAEIIYPIMDKSRTRLALII 173
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 173 RESGLRTRTGSNIDCEKLRFRFSSLFHFMVEVKGDLTAKKWLALLELA-RQDH 231
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 174 --DSIPRTGAEVDTGTMTLLQNLGYSVDVKKNLTAADMTELEAFARPEHKTSD 231
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 232 VVILSHG-----COASHL-QFFGAVYGTDCFPVSVEKIVNIENGTSCPSLGGKPK 285
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 LVFMSHGIREGICGKKHSEQVPDI-----LQLNAIFNMLTNKCPSLKDKPKV 283
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 286 ACGGEQKHGHFEVASTSPEDESP-----GSNPEPDATPFQEGRLTFDOLD 333
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 284 ACRG-----DSPGVVWFKDSVGVSGNLSLPTTEBFED-----DAIK 319
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 334 SLPTSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLR 393
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 320 KAHIEKDFIAFCSTFDNVSWRHPTMGVSFIGRLIEHMQEYACSCDVEIFRK 379
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 394 KGIYKQMP 401
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 380 PDGRAQMP 387
```

Search completed: August 3, 2004, 08:55:08
Job time : 20 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:15 ; Search time 41 Seconds
(without alignments)
3201.355 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRCLRLVEEL.....YKMPGCFNLRKLLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1647	75.6	454	11	Q8C3Q9
2	1645	75.5	454	11	Q9JHK1
3	1645	75.5	454	11	Q9ROT0
4	1642	75.3	453	11	Q8C3Q0
5	1336	61.3	393	11	Q9ROS9
6	1093	50.1	383	11	Q9PM88
7	1048.5	48.1	399	13	Q9IB63
8	1000.5	45.9	403	13	Q9OWU0
9	613	28.1	229	11	Q7TQC1
10	485	22.2	177	11	Q920G4
11	449	20.6	426	5	Q816Y2
12	443	20.3	423	13	Q9IB67
13	437	20.0	313	11	Q8CHV5
14	435	20.0	316	5	Q817B0
15	424	19.4	482	11	Q9JHX4
16	421	19.3	328	5	Q81TP3

17	420	19.3	277	6	Q9SND5
18	419	19.2	277	6	Q8MJU1
19	418	19.2	280	13	Q8JGM9
20	414	19.0	452	11	O55194
21	413	18.9	280	13	Q8JG42
22	411	18.9	452	11	Q8K241
23	410	18.8	452	11	Q8C9H7
24	406	18.6	435	4	Q9BUP7
25	402.5	18.5	318	13	Q9IB65
26	401	18.4	277	6	Q8MKI5
27	401	18.4	277	6	Q8MTC3
28	396	18.2	283	13	Q93417
29	393	18.0	282	13	Q98UI8
30	387.5	17.8	482	13	Q90WU1
31	384	17.6	280	13	Q8JIS9
32	383.5	17.6	476	13	Q918J3
33	378.5	17.4	290	13	Q8JIS8
34	369	16.9	415	13	Q801M6
35	369	16.9	419	13	Q7ZXD2
36	362.5	16.6	303	11	O88550
37	362	16.6	182	6	O77623
38	344.5	15.8	522	4	Q8IUP5
39	333	15.3	289	5	Q86ELO
40	330.5	15.2	400	5	Q81TP2
41	330	15.1	417	5	Q9YIU6
42	326.5	15.0	304	13	O93415
43	322	14.8	276	11	Q99M47
44	321	14.7	276	11	Q9D089
45	318	14.6	520	13	Q9IB62

ALIGNMENTS

RESULT 1
Q8C3Q9 PRELIMINARY; PRT; 454 AA.
AC Q8C3Q9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK085095; BAC39365.1; --
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; Cintracellular; IEA.
DR GO; GO:0016329; Fapoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASE; 1.
DR PROSITE; PS50209; CARD; 1.

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DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 49979 MW; 438A67EA6A6EE78 CRC64;

Query Match 75.5%; Score 1647; DB 11; Length 454;
Best Local Similarity 71.1%; Pred. No. 3.1e-139;
Matches 325; Conservative 28; Mismatches 63; Indels 38; Gaps 2;

QY 1 MDEADRLRRCLRLVEELQVDQLDWLLSRELFRPHMIEDIORAGSGRRDQARQLII 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MDEADRLRRCLRLVEELQVDQLDWLLSRELFRPHMIEDIORAGSGRRDQARQLV 60
QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKL----- 98
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKL----- 98
QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKL----- 98
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKL----- 98
QY 99 -----SKPTLENLTPVLRPE-----IRKPEVLRETPTPRVDIGSGFGDVGAL 142
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 -----SKPTLENLTPVLRPE-----IRKPEVLRETPTPRVDIGSGFGDVGAL 142
QY 121 SKEQKVVKLDPSQALGNLTPVLGPPELWFLTRLRPEVLTPETPRVDIGSGRAHDVCTP 180
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 SKEQKVVKLDPSQALGNLTPVLGPPELWFLTRLRPEVLTPETPRVDIGSGRAHDVCTP 180
QY 143 ESLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVVE 202
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 ESLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVVE 202
QY 181 GKIERHADMYATLSDPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVVE 240
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 GKIERHADMYATLSDPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVVE 240
QY 203 VKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLQPPGAVYGTGCPVSVK 262
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
203 VKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLQPPGAVYGTGCPVSVK 262
QY 241 VKNDLTAKKMWLALMAHRDHRALDCFVVVILSHGCOASHLQPPGAVYGTGCVSIEK 300
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
241 VKNDLTAKKMWLALMAHRDHRALDCFVVVILSHGCOASHLQPPGAVYGTGCVSIEK 300
QY 263 IVNIFNGTSCPSLGGKPKLFIQACGGEKDHGFVASTSPEDSPGNSPDPATPFQEG 322
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
263 IVNIFNGTSCPSLGGKPKLFIQACGGEKDHGFVASTSPEDSPGNSPDPATPFQEG 322

RESULT 2
Q9JHK1 PRELIMINARY; PRT; 454 AA.
AC Q9JHK1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-9 (Caspase-9 long isoform).
GN RNCASP9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Cao G., Chen D., Pei W., O'Horo C., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
in Neuronal Cell Death During Brain Development and Transient Cerebral
Ischemia.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Itoh T., Itoh A., Pleasure D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Chen D., Graham S., Simon R.P., Chen J.;
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Db 301 IVNIFNGTGCPSLGKPKLFFIQACGGEQKHGFVASTSPEDSPGSGSWYVETLDDIFQWASEDLQS 360
QY 323 LRTFDQDLDAISSLPDSDFVSYSTPFGFVSWRDPKSGSWYVETLDDIFQWASEDLQS 382
Db 361 PRTLDQDLDAVSSLPDSDFVSYSTPFGFVSWRDPKSGSWYVETLDDIFQWASEDLQS 420
QY 383 LLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416
Db 421 LLLRVANAVSEKGYKQIPGCFNLRKLFKFTS 454

RESULT 3
Q9ROT0
ID Q9ROT0 PRELIMINARY; PRT; 454 AA.
AC Q9ROT0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
caspase-9.";
RL Biochem. Biophys. Res. Commun. 264:550-555(1999).
DR EMBL; AB019600; BAA86895.1; -.
DR PIR; JC7123; JC7123.
DR HSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50051 MW; 4614989AF923850F CRC64;

Query Match 75.5%; Score 1645; DB 11; Length 454;
Best Local Similarity 71.6%; Pred. No. 4.6e-139;
Matches 325; Conservative 28; Mismatches 63; Indels 38; Gaps 2;

QY 1 MDEARRLLRRCRLRLVEELQVDLWVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEARRLLRRCRLRLVEELQVDLWVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRINRQAKL----- 98
Db 61 DLETRGRQALPLFISCLEDTGGTASLQSGRQAKQDPEAVKLDHLVPVVLGPMGLT 120
QY 99 -----SKPTLENITPVVLRPE-----IRKPEVLRPTPRPDVIGSGGFDVGAL 142
Db 121 AKEQRVVKLEPSQAVGNLTPVVLGPEELWPARLKPEVLRPTPRPDVIGSGGHDVCVP 180

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QY 143 ESURGNADLAIYILSMPECGHCLINNNVNFRESGLRTRTGSNIDCEKLRFRFSSHFVME 202
Db 181 GKIRGHADMAYTLDSDFCGHCLINNNVNFPCSSGLGTRTGSNLDRLKLEHFRWLRFVME 240
QY 203 VKGDLTAKKVVALLLELARGDHALDCVWVILSHGCOASHLOFPFGAVYGTGDCPVSVEK 262
Db 241 VKNDLTAKKVVMTALMEMAHNRHALDCFVVVILSHGCOASHLOFPFGAVYGTGDCSVSIEK 300
QY 263 IVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFVASTSPEDSPGSGSWYVETLDDIFQWASEDLQS 322
Db 301 IVNIFNGSGCPSLGKPKLFFIQACGGEQKHGFVASTSPGSGSWYVETLDDIFQWASEDLQS 360
QY 323 LRTFDQDLDAISSLPDSDFVSYSTPFGFVSWRDPKSGSWYVETLDDIFQWASEDLQS 382
Db 361 PRTLDQDLDAVSSLPDSDFVSYSTPFGFVSWRDPKSGSWYVETLDDIFQWASEDLQS 420
QY 383 LLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416
Db 421 LLLRVANAVSEKGYKQIPGCFNLRKLFKFTS 454

RESULT 4
Q8C3Q0
ID Q8C3Q0 PRELIMINARY; PRT; 453 AA.
AC Q8C3Q0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/60; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK085152; BAC39378.1; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
FT NON TER
SQ SEQUENCE 453 AA; 49847 MW; 8F7D1C50F7ABA69F CRC64;

Query Match 75.3%; Score 1642; DB 11; Length 453;
Best Local Similarity 71.5%; Pred. No. 8.6e-139;
Matches 324; Conservative 28; Mismatches 63; Indels 38; Gaps 2;

QY 2 DEARRLLRRCRLRLVEELQVDLWVLLSRELFRPHMIEDIQAGSGSRDQARQLII 61

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DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 383 AA; 42319 MW; 3C5D217C3100FF25 CRC64;

Query Match
Best Local Similarity 50.1%; Score 1093; DB 11; Length 383;
Matches 220; Conservative 22; Mismatches 47; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVEELQVDQLNDVLLSRLFRPHMIEDIQRAGSGRRDQARQLII 60
Db 1 MEADRLQLRCRLRLVRELVQVLELMDALLSRLFRPHMIEDIQRAGSGRRDQARQLVI 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAKLSKPTLENLTPVVLREIRKPEV 98
Db 61 DLETRGQALPRFISCLEDTGQSLASFLSSQAAKQDPEAVTLDHLVPPVVLGPMGLK 120
QY 99 -----SKPTLENLTPVVLRE-----TRKPEVLRPETPRPVVDIGSGFGDVGAL 142
Db 121 SKEQKVVLKDPSPQALGNLTPVVLGPEELWPTLRPEVLTPTPRPVVDIGSGRAHDVCTP 180
QY 143 ESLRGNADLAYILSMPCGHCLLIINNVPFCRESGLRTRGSLNIDCEKLRFRPSLHMVE 202
Db 181 GKIERHADWYTLDSPCGHCLLIINNVPFCPSGLSTRIGSHVDCBKLRHRCWLRFMVE 240
QY 203 VKGDLTAKKWLALLELRLAQDGHGALDCCVVVILSHGCOASHLOFPQAVVGTGDCPVSVEK 262
Db 241 VKNDLTAKKWTALMEWAHRDHALDCFVVVILSHGCOASHLOFPQAVVGTGDCSVSIER 300
QY 263 IVNIFNGTSCPSLGKPKLFFIIQACGG 289
Db 301 IVNIFNGTSCPSLGKPKLFFIIQACGG 327

RESULT 7
Q91B63 PRELIMINARY; PRT; 399 AA.
AC Q91B63
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:000693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILICENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match
Best Local Similarity 48.1%; Score 1048.5; DB 13; Length 399;
Matches 216; Conservative 67; Mismatches 113; Indels 21; Gaps 6;

QY 1 MDEADRLRLRCRLRLVEELQVDQLNDVLLSRLFRPHMIEDIQRAGSGRRDQARQLII 60
Db 1 MEQELRDIIILRRNRVRLVQSLQVKELWDLIVRGVFSNDMIEIQR--EGTRDQARKLLV 58
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAKLSKPTLENLTPVVLREIRKPEV 120
Db 59 ELETSGSQAFPLFLCLCKETAQHDLDLADFLQSD--SGTRVLQPTPTTSP--VLKP--LPKA 113
QY 121 LRPETPRPVVDIGSGFGDVGALESRLG--NADLAYILSMPCGHCLLIINNVPFCRESGLR 178
Db 114 EPAEYP-----ARETRSRKGTLDKDKDYPMSDDPIGFCIIINNMFHECTGLS 161
QY 179 TRTGSNIDCEKLRRRPSLHFVVEKGDITAKKWLALLELRLAQDGHGALDCCVVVILSHG 238
Db 162 TRTGSIDIDRDLKLRNRMSFHFVTVKDNLTGQAMHDHLQALADQDHSQDCLLVILSHG 221
QY 239 COASHLOFPQAVVGTGDCPVSVEKIWNIFNGTSCPSLGKPKLFFIIQACGGKDHGFV 298
Db 222 CETRHQIFGFGVYGTGIRIPVERIVSYFNGSKPCSLRQPKFIILQACGGDKQKCEV 281
QY 299 ASTSPEDSPGNPEPDATPQEGLTFDQLDAISSLTPTSDIFVSYSYTFPGFVSWRDPK 358
Db 282 TSETPTPLSPTSLQSDATPVFSGEDRDEVDAVSNIPSTDILVSYSYTFPGVSVWRDXH 341
QY 359 SGSWVYVETLDDIFEQWHSDEIQLLLRVANAVSVKGIYKQMPGCFNFKKLLFFKT 415
Db 342 TGSWYVEVLDSVLAHHAADDILQSLVWVADGVSSKGYKQIPGYFNFLRKRFYFKT 398

RESULT 8
Q90WU0 PRELIMINARY; PRT; 403 AA.
AC Q90WU0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgham J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR001393; Mitoch carrier.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
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OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Eukaryota;
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344144; CAC83013.1; -.
DR GO; GO:00030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR Pfam; PF00656; Peptidase_C14.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR SEQUENCE 426 AA; 48024 MW; 713B5EC82EBD0C1 CRC64;

Query Match 20.6%; Score 449; DB 5; Length 426;
Best Local Similarity 32.6%; Pred. No. 1.2e-31;
Matches 127; Conservative 57; Mismatches 150; Indels 56; Gaps 14;

QY 53 DOARQLIIDLTRGSQALPLFISCL---EDTGQDM---LASFLRTNRQAGKLSKPTLENL 106
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 54 EAADELKALRRDSSVLDILVECLAQEQEANADLIKKIRSF-PEKPRPPPPPTIDS- 111

QY 107 TPVVLRLPE---IRKPEVLRLPTPRPDVIGSGGFGVGALESRLGNADLAYILSMPCGH 162
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 TPVTYDWPAPAIATATSHPIPPPEGT-----DAGRKD-----AYKMSRPRGM 159

QY 163 CLIIINNVPFRESGLRTGTSNIDCEKLRRRRSSLHFMVVEKGDLTAKKWLALLELAHQ 222
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 ALIINNRF--TCGMKERVGTDKDAENLYGLFNWLGMATIRKNTLTKAMTEFEDLARR 217

QY 223 DHGALDCCVVVILSHGQASHLOFPGAVYGTDCGPVSKIVNIENGTSCLSGKPKLF 282
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 DHSAYDCVVVAILTHG-----ISGRLYSTDGLIPVEDLTKYFDGVNRPRLIGKPKVF 270

QY 283 FTAQCGGQKHGFVAVASTSPEDSPGSPNPEPDATPFQGLRTFDQ-----LDA----- 331
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 271 VVQACRGKGFYGVSESTDGESVNV---KETANEMME--KQFDKWEKALDADETDGG 325

QY 332 ---ISLPPSPDIFVSYSYTFPGFVSWRDPKSGSWVETLDDIFEQWAHSEDLSLILRVA 388
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 326 GYSREALPTEADFVLAYATVPGVSWRNSEYGSWFIKAFVDITMRDLASKEHFMDILTEVN 385

QY 389 NAVSV-----KGIYKQMPGCFNLRKKLPFK 414
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 386 RKVAYDFQSRGRNKQIPAPVTMLTRKLYPR 415

RESULT 12
Q9IB67
ID Q9IB67 PRELIMINARY; PRT; 423 AA.
AC Q9IB67;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-2.
GN XCASPASE-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;

"Structure, expression and function of the Xenopus laevis caspase family.";
J. Biol. Chem. 275:10484-10491 (2000).
EMBL; AB038168; BAA94746.1; -.
MEROPS; C14.006; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0030693; F:caspase activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; ILIBCEZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASc; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
SEQUENCE 423 AA; 47123 MW; E91EB1FD133F01FD CRC64;

Query Match 20.3%; Score 443; DB 13; Length 423;
Best Local Similarity 31.9%; Pred. No. 4e-31;
Matches 135; Conservative 59; Mismatches 167; Indels 62; Gaps 14;

QY 1 MDEARRLLRCRLRLVBELOVDLQVLDVLLSRLFRPHMIEDIQAGSGRRDQARQ--L 58
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 MOQHRKALQRLRVSLASEMIEELLHLVSSLEITNNMHSNM---AYRSDYACNVAL 60

QY 59 IIDLTRGSQALPLFISCLDGTQDMLA-----SELTNRQAGKLSKPTLENLT 107
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LMLLPKRGPRAPSAFCNALHSTNQHLAQOQVEKALLOBEFITSKVHGSFPLPQES-- 118

QY 108 PVLRLP-----EIRKPEVLRLPTPRPDVIGSGGFGVGALESRLGNADLAYILSMPCG 161
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 -TLSPRGQICREYREESIDDGDPVTVOLCSVNF-----YITHCQAYKMHSCPRG 169

QY 162 HCLINNVPFRESGLRTGTSNIDCEKLRRRRSSLHFMVVEKGDITAKKWLALLELA 220
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 RALLISNVKF-BTPDLRYRCGGEVDLASLEKLFSSLGYPQVDRCLNQAQSMMSQLGAFSA 228

QY 221 RDHGALDCCVVVILSHGQASHLOFPGAVYGTDCGPVSKIVNIENGTSCLSGKPK 280
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 229 LPVHSALDCCVVVAILSHG-----LDGAVYGTDDKLVQEQVFTALDNNAHCPQLQNRK 281

QY 281 LFFIQACGQKHGFVAVASTSPEDSPGSPNPEPDATPFQGLRTFDQLDAISSLPSPD 340
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 282 MFFIQACRGEETDRGVQDQDQREQSGSPGCE-QSDA-----GREDKVRLPTQSD 330

QY 341 IFVSYSTPFGFVSWRDPKSGSWVETLDDIFEQWAHSEDLSLILRVAN-AVSVGIYKQ 399
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 MICAYACLKGTSLRNTRKSGFWQDLVSFVSQ--HSDK-----THVADMLVKVNALIKE 383

QY 400 MFG 402
Db 384 REG 386

RESULT 13
Q8CHV5
ID Q8CHV5 PRELIMINARY; PRT; 313 AA.
AC Q8CHV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3, apoptosis related cysteine protease (Fragment).
GN CASP3.
```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038825; AAH38825.1; -.
DR MGD; MGI:107739; Casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IILBCENZME.
DR SMART; SMO0115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Protease.
FT NON TER
SQ SEQUENCE 313 AA; 35174 MW; 96E98A1F04E769FC CRC64;

Query Match 20.0%; Score 437; DB 11; Length 313;
Best Local Similarity 31.5%; Pred. No. 9.1e-31;
Matches 106; Conservative 52; Mismatches 123; Indels 56; Gaps 5;

QY 87 SFLTRNRQAGKLSKPTLENITPVVLRPEIRKPEVLRPETPRPDIGSGFGDVGALBSLR 146
Db 21 SVLRGAWNGTLRKVTENNKTSVDSKSIINFEVKTHGSKSVDSGI----- 67

QY 147 GNADLAYILSMPEGCHGLIINNVPFCESGLTRTSGNIDCEKLRFRFSSLHFVVEVKGD 206
Db 68 -YLDSSYKMDYPENIGICIIINNKFHKSSTGMSRSRGTVDAAANLRETFMGLKYQVRNKND 126

QY 207 LTAKKMWLALLELARQDHGALDCCVVILSHGQASHLPFGAVGTGDCGSPVSEKIVNI 266
Db 127 LTRDILLELMDSVSKEDHKSRSFVCVILSHGDE-----GVITYGNG-FVELKXLTSF 178

QY 267 FNGTSCPSLGKPKLFFIQACGGEQKDHGPEVASTSPEDSPGSPNPEPDATPFQEGRLTF 326
Db 179 FRGDYCESLTKGPKLFFIQACRGTELDGCIETDSGTDEM----- 218

QY 327 DQLDATSLPTPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFQWHAHSEDLQSLLLR 386
Db 219 ----ACQKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCSMLKLYAHKLEFPHILTR 274

QY 387 VANAVSVK-----GIYKMPGCFNLRKLLF 413
Db 275 VNRKVATEFFESFLDSTFFHAKQIPICVISMLTKEYLF 311

RESULT 14
Q817B0
ID Q817B0 PRELIMINARY; PRT; 316 AA.
AC Q817B0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Eukaryophora; Geodidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA Wiens M., Saenger H., Kraeko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";

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RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417903; CAD10676.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IILBCENZME.
DR SMART; SMO0115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 316 AA; 35319 MW; 33A46BCE6C3F9B7 CRC64;

Query Match 20.0%; Score 435; DB 5; Length 316;
Best Local Similarity 35.1%; Pred. No. 1.4e-30;
Matches 113; Conservative 44; Mismatches 121; Indels 44; Gaps 9;

QY 111 LRPEIRKPEVLRPETPRPDIGSGFGDVGALBSLRGNADLAYILSMPEGCHGLIINN 170
Db 10 VRLLIAPTATSHPPIPPPPEGT-----DAGRKD-----AYKMSRRPRGMALII 57

QY 171 FCRESGLRTRTSGNIDCEKLRFRFSSLHFVVEVKGDITAKKMWLALLELARQDHGALDCC 230
Db 58 F--TCGMKERVGDGDAENLYGLFNNLGMATIRKDNLTGKATREFEDLARRDHSAYDCV 115

QY 231 VVILSHGQASHLPFGAVGTGDCGSPVSEKIVNIPNGTSCPSLGKPKLFFIQACGGE 290
Db 116 VVAILTHG-----ISGRLYSTGDLIPVEDLTKYFDGVNRPESLIGKPKVFFVQACRG 168

QY 291 QKHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQ-----LDA-----ISSLP 336
Db 169 KFDYGVESSTDEGESVN---KETANEMME---KQFDKVVKEKALDADETDGGGYSREALP 223

QY 337 TPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFQWHAHSEDLQSLLLRVANAVSV-- 393
Db 224 TEADFVLAYATVPGYYSWRNSKEYSWFIKAFVDTMRDLASKEHFMDILTEVNRKVAYDFQ 283

QY 394 -KGIIYKMPGCFNLRKLLFFK 414
Db 284 SGRNRKQIPAPVTMLTRKLYFR 305

RESULT 15
Q9JHX4
ID Q9JHX4 PRELIMINARY; PRT; 482 AA.
AC Q9JHX4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-8.
GN CASP8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Graham S.H., Chen D., Chen J.;
RT "Molecular cloning and characterization of rat caspase-8: Its
RT implication in delayed neuronal cell death after ischemia.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279308; AAF87778.1; -.
DR EMBL; AF280372; AAK83055.1; -.
DR HSSP; Q15806; IQDU.

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DR MEROPS; C14.009; --
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 482 AA; 55339 MW; 82B4A29330C53264 CRC64;

Query Match      19.4%; Score 424; DB 11; Length 482;
Best Local Similarity 29.9%; Pred. No. 2.4e-29;
Matches 138; Conservative 60; Mismatches 173; Indels 90; Gaps 14;

QY 15 RLVEE--LQVDQLMDVLLSRELPRPHMEDIQRAGSGRRDQARQLIIDLETGSOALPL 72
Db 47 RLQEGMLEEDNL--SPFKELLFHSRRDLISRLVLSKSPBEMVRELQVLGKAQVAYRVM 104

QY 73 FISCLENTGQDMLASF---LRTNRQAGKLSKPTLENLTPVLRPEIRKPEVL----- 121
Db 105 LFKLSMDMDKEDLKSPEFLLIETPKCKLQ---DNSLLDIFVEMEKRTILAENNLVTL 160

QY 122 -----RPETPRPVDIGSGG-----FGDVGALESL 145
Db 161 KSICFRVNRSLGRIDDIYERSSTERRMSTEGBELPVSVLDEVITKQMDMWDSPGEQSE 220

QY 146 RGNADLAYILSMPEPCGHCLINNVF--CRE-----SGLRTRTGSNIDCEKLRFRFSLH 198
Db 221 SLNSDNVYQMKSPRGYCLIFNNNFSKAREDI PKLSNMEDRKGTNYDEALSKITKELH 280

QY 199 FMVEVKGDLTAKKWLALLLELARQDHGALDCCVVWILSHGCQASHLQFPGAVYGTGCPV 258
Db 281 FEIVSPSDCTASQIHEVLVSYSQKHGKDCFCICILSHGDK-----GIVYTDGKEA 333

QY 259 SVEKIWNIFNGTSCPSLGGPKLFFIQACGGEQKHGFEVASTSPEDSEPGSNPEPDATP 318
Db 334 SIYELTSYFTGSKCPSLAGPKIFFIQACQG---NNFQKAV-----PVPEDTG 378

QY 319 F-QEGLRTFDQLDAISLPTSPDIFVSYSTFPFGVSWRDPKSGSWYVETL-DDIFEQWAH 376
Db 379 LEQHVLEEDSSSYKXVIPEADFLGMATVKNVCVSYRDTGTGTWTYIQLCSLRERCPR 438

QY 377 SEDLQSL---LRVANAVSVKGIYKQMPGCFNFKLKLFF 413
Db 439 GEDILSILGTGVNVDVSNKPNRWGMQMPQPIETLRKKLFF 479
```

Search completed: August 3, 2004, 08:54:40
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:14 ; Search time 55 Seconds
(without alignments)
2137.087 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKQPGCFNFKKLPFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	2 AAW39209	Aaw39209 Human ICE
2	2180	100.0	416	4 AAE00606	Aae00606 Human cas
3	2166	99.4	416	6 ADA10646	Ada10646 Human cas
4	2158	99.0	416	6 ADA10674	Ada10674 Human cas
5	2157	98.9	416	2 AAY21723	Aay21723 Amino aci
6	2157	98.9	416	5 ABJ01124	Abj01124 Human cas
7	2153	98.8	416	4 AAG67375	Aag67375 Amino aci
8	2153	98.8	416	4 AAU08315	Aau08315 Human asp
9	2153	98.8	416	4 AAE08938	Aae08938 Mammalian
10	2153	98.8	416	4 AAB84374	Aab84374 Amino aci
11	2153	98.8	416	6 ABB82738	Abb82738 Human cas
12	2153	98.8	416	8 ADE52020	Ades2020 Human mam
13	2150	98.6	416	6 ADA10675	Ada10675 Human cas
14	2144	98.3	416	6 ADA10676	Ada10676 Human cas
15	2069.5	94.9	401	6 ADA10677	Ada10677 Human cas
16	1288	59.1	266	4 AAE00620	Aae00620 Human cas
17	1083	49.7	203	4 AAW39208	Aaw39208 Human ICE
18	468	21.5	93	5 ABJ04760	Abj04760 Caspase-9
19	420	19.3	277	4 AAG78712	Aag78712 Pig caspa
20	418	19.2	249	3 AAB26763	Aab26763 Human cas
21	418	19.2	277	2 AAW00372	Aaw00372 Apopain C
22	418	19.2	277	2 AAW16600	Aaw16600 Apopain C
23	418	19.2	277	2 AAR95831	Aar95831 Human int
24	418	19.2	277	2 AAW00677	Aaw00677 Pro-Yama
25	418	19.2	277	2 AAW41688	Aaw41688 Amino aci

26	418	19.2	277	2 AAY21717	Aay21717 Amino aci
27	418	19.2	277	4 AAU05394	Aau05394 Human cas
28	418	19.2	277	4 AAU05395	Aau05395 Mouse cas
29	418	19.2	277	4 AAE00600	Aae00600 Human cas
30	418	19.2	277	5 ABG30904	Abg30904 Human mem
31	418	19.2	277	5 ABJ01218	Abj01218 Human cas
32	418	19.2	277	6 AAO19867	Aao19867 Bacteriop
33	418	19.2	277	7 ADD25641	Add25641 Binding d
34	418	19.2	277	7 ADE63082	Ade63082 Human Pro
35	416.5	19.1	245	4 AAB59579	Aab59579 Human cas
36	414.5	19.0	261	4 AAE00610	Aae00610 Chimeric
37	414	19.0	241	4 AAB98654	Aab98654 Caspase-3
38	414	19.0	452	7 ADB79812	Adb79812 Rat caspa
39	414	19.0	452	7 ADE63000	Ade63000 Rat Prote
40	411	18.9	452	5 ABB10110	Abb10110 Mouse cas
41	409	18.8	277	2 AAW47089	Aaw47089 Rat inter
42	409	18.8	277	7 ADE63080	Ade63080 Rat Prote
43	409	18.8	435	2 AAR66771	Aar66771 Human int
44	409	18.8	435	2 AAR98462	Aar98462 Human Ice
45	409	18.8	435	2 AAW26274	Aaw26274 Cell deat

ALIGNMENTS

RESULT 1

AAW39209

ID AAW39209 standard; peptide; 416 AA.

AC AAW39209;

XX

DT 18-MAY-1998 (first entry)

XX Human ICE LAP-6 polypeptide.

DE

XX ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;

KW viral infection; tumour; inflammation; osteoporosis; AIDS; human;

KW Alzheimer's disease.

XX Homo sapiens.

OS

XX EP808904-A2.

PN

XX 26-NOV-1997.

PD

XX 19-MAY-1997; 97EP-00303397.

PF

XX 20-MAY-1996; 96US-0017949P.

PR

XX 23-MAY-1996; 96US-0020344P.

PR

XX 05-JUN-1996; 96US-0018961P.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

XX Dixit VM, He W, Ruben SM, Kikly KK;

PI WPI; 1998-001790/01.

XX N-PSDB; AAW09401.

DR

XX DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -

PT useful to develop products to treat, e.g. viral infection, tumour,

PT Alzheimer's disease, inflammation, osteoporosis and AIDS.

XX Claim 4; Fig 1; 44pp; English.

PS

XX This is a human interleukin-1 beta converting enzyme apoptosis protease-6

CC (ICE LAP-6) polypeptide. The ICE LAP-6 polypeptide and agonists to the

CC polypeptide can be used to induce apoptosis, e.g. as an antiviral or

CC antitumour agent, control embryonic development and tissue homeostasis

CC and the roles of such factors in dysfunction and disease. Antagonists

CC which inhibit the activity of the ICE LAP-6 polypeptide can be used to

CC treat, Alzheimer's or Parkinson's disease, rheumatoid arthritis, septic

CC shock, sepsis, stroke, chronic, acute or central nervous system
CC inflammation, osteoporosis, ischaemia reperfusion injury, cell death
CC associated with cardiovascular disease, polycystic kidney disease,
CC apoptosis of endothelial cells in cardiovascular disease, degenerative
CC liver disease, multiple sclerosis, cerebellar degeneration, ischaemic
CC injury, myocardial infarction, acquired immunodeficiency syndrome (AIDS),
CC myelodysplastic syndrome, aplastic anaemia, male pattern baldness and
CC head injury damage. They can also be used for detection and diagnosis
XX
SQ Sequence 416 AA;

Query Match 100.0%; Score 2180; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 1e-219;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 120
Db 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 60

QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 120

QY 121 LRPETPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLLIINNVMFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLLIINNVMFCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRRFSSSLHFMVEVKGDLTAKQWVLLALLELARDHGALDCCVVVILSHGCO 240
Db 181 TGSNIDCEKLRRLRRFSSSLHFMVEVKGDLTAKQWVLLALLELARDHGALDCCVVVILSHGCO 240

QY 241 ASHLQFPQAVYGTDCGCPVSVKEKVINI FNGTSCPSLGGKPKLFFIQACGGEQKHGFEVAS 300
Db 241 ASHLQFPQAVYGTDCGCPVSVKEKVINI FNGTSCPSLGGKPKLFFIQACGGEQKHGFEVAS 300

QY 301 TSPEDSGSPNPEPDATPFQGLRFTDQDLSLPTSDIFVSYSTPFGVSVWRDPKSG 360
Db 301 TSPEDSGSPNPEPDATPFQGLRFTDQDLSLPTSDIFVSYSTPFGVSVWRDPKSG 360

QY 361 SWYVETLDDIFQWHAHSEDLSLLRLVANAVSVKGIYQKMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFQWHAHSEDLSLLRLVANAVSVKGIYQKMPGCFNLRKLLFFKTS 416

RESULT 2
AAE00606
ID AAE00606 standard; protein; 416 AA.
XX
AC AAE00606;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human caspase-9, alternative version.
XX
KW Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6;
KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
KW tumour; cathepsin B; urokinase; proliferation; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 28 /note= "Encoded by GCC; Ala is present in the sequence
FT shown in page 105-107 (AAE00620)"
FT Misc-difference 96 /note= "Encoded by GCA; Ala is present in the sequence
FT shown in page 105-107 (AAE00620)"
FT Misc-difference 139, 290 /note= "Encoded by GTCGAG; Amino acid residues from
FT position 140 to 289 present in this sequence are not
FT found in the sequence shown in page 105-107 (AAE00620)"
FT Cleavage-site 315..316 /label= Proteolytic_cleavage_site
FT

FT Cleavage-site 330..331 /label= Proteolytic_cleavage_site
XX
FN W0200129232-A2.
XX
PD 26-APR-2001.
XX
PF 19-OCT-2000; 2000MO-US028941.
XX
PR 20-OCT-1999; 99US-0160559P.
PR 14-AUG-2000; 2000US-0225564P.
XX
PA (SCIO-) SCIOS INC.
XX Cordell B, Li Y;
XX
PI
XX WPI; 2001-290920/30.
DR N-PSDB; AAD03916.
XX
PT Novel fusion polypeptide comprising first and second caspase subunit
PT separated by cleavage site not associated in nature with caspase subunit,
PT useful for cloning gene encoding enzymes involved in proteolytic
PT cleavage.
XX
PS Claim 4; Fig 18; 116pp; English.
XX
CC The present sequence is an alternative version of human Caspase-9 also
CC known as interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases
CC are a family of cysteine proteases, that participate in the initiation
CC and execution of apoptosis. Caspases exist as pro-enzymes, activated by
CC cleavage into a large and small subunit, occurring after specific
CC aspartic acid residues within the pro-enzyme sequence. The present
CC invention relates to a method for functional cloning of genes encoding
CC proteins or enzymes involved in proteolytic cleavage. The invention is
CC based on the use of caspase expression cassettes comprising the coding
CC sequence of a proteolytic cleavage site flanked by sequences encoding two
CC caspase subunits. A fusion polypeptide comprising a first and a second
CC caspase subunit, separated by a cleavage site not associated in nature,
CC is useful for cloning gene encoding enzymes involved in proteolytic
CC cleavage. An expression cassette containing fusion polypeptide is used to
CC identify a mutant cell line deficient in an enzyme of interest and is
CC also useful for diagnosis and suppression of proliferation or metastases
CC of a tumour cell characterised by overexpression of a polypeptide (e.g.
CC cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
CC encoding fusion polypeptide is used in gene therapy. Note: This sequence
CC SEQ.ID.NO.18 is stated as being the same as that shown in page 105-107
CC (See AAE00620) in the specification. However these sequences differ at
CC several positions
XX
SQ Sequence 416 AA;

Query Match 100.0%; Score 2180; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1e-219;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 60
Db 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 60

QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPKPEV 120

QY 121 LRPETPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLLIINNVMFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLLIINNVMFCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRRFSSSLHFMVEVKGDLTAKQWVLLALLELARDHGALDCCVVVILSHGCO 240
Db 181 TGSNIDCEKLRRLRRFSSSLHFMVEVKGDLTAKQWVLLALLELARDHGALDCCVVVILSHGCO 240

QY 241 ASHLQFPQAVYGTDCGCPVSVKEKVINI FNGTSCPSLGGKPKLFFIQACGGEQKHGFEVAS 300
XX

Db 241 ASHLQFPGAVYGTGCPVSVKIVNFGTSCPSLGGKPKLFFIQACGGKQDHGFEVAS 300
 Qy 301 TSPDESPGSPNPEDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGFVSWRDPKSG 360
 Db 301 TSPDESPGSPNPEDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGFVSWRDPKSG 360
 Qy 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 3

ADA10646
 ID ADA10646 standard; protein; 416 AA.

XX AC ADA10646;

DT 06-NOV-2003 (first entry)

DE Human caspase-9 protein.

XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease.

XX Homo sapiens.

XX US2002160975-A1.

PN 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

PR 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

DR N-PSDB; ADA10661.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

PS Claim 36; Page 25-26; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,

CC identifying a compound that inhibits the peptide or polypeptide
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the full length caspase-9 protein.

XX SQ Sequence 416 AA;

Query Match 99.4%; Score 2166; DB 6; Length 416;
 Best Local Similarity 99.3%; Pred. No. 3e-218;
 Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLWDALLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 Db 1 MDEADRLRLRCRLRLVEELQVDQLWDALLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 Qy 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNQAGKLSKPTLENLTPVLRPEIRKPEV 120
 Db 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNQAGKLSKPTLENLTPVLRPEIRKPEV 120
 Qy 121 LRPEPRPVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVMFCRESGLRTR 180
 Db 121 LRPEPRPVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVMFCRESGLRTR 180
 Qy 181 TGSNIDCEKLRFRFSSLHFHVEVKGDLTAKQWVALLLELARDHGAIDCCVWILSHGQQ 240
 Db 181 TGSNIDCEKLRFRFSSLHFHVEVKGDLTAKQWVALLLELARDHGAIDCCVWILSHGQQ 240
 Qy 241 ASHLQFPGAVYGTGCPVSVKIVNFGTSCPSLGGKPKLFTQACGGKQDHGFEVAS 300
 Db 241 ASHLQFPGAVYGTGCPVSVKIVNFGTSCPSLGGKPKLFTQACGGKQDHGFEVAS 300
 Qy 301 TSPDESPGSPNPEDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGFVSWRDPKSG 360
 Db 301 TSPDESPGSPNPEDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGFVSWRDPKSG 360
 Qy 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 4

ADA10674

ID ADA10674 standard; protein; 416 AA.

XX AC ADA10674;

XX DT 06-NOV-2003 (first entry)

XX DE Human caspase-9 protein D315A mutant.

XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; mutin.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 315 /note= "Wild-type Asp substituted by Ala"

XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGKLSKPTLENLTPVILRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGKLSKPTLENLTPVILRPEIRKPEV 120
QY 121 LRPTPRVDITGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLLIINNWFRCRESGLRTR 180
DB 121 LRPTPRVDITGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLLIINNWFRCRESGLRTR 180
QY 181 TGSNIDCEKLRFRSSLSHFVVEVKGDLTAKMWLALLELARQDHGALDCCVVWILSHGCQ 240
DB 181 TGSNIDCEKLRFRSSLSHFVVEVKGDLTAKMWLALLELARQDHGALDCCVVWILSHGCQ 240
QY 241 ASHLQFPFCAVVTGDCPVSVEKIVNIENGTSCPSLGGKPKLFFIOACGGEQKDHGFVEAS 300
DB 241 ASHLQFPFCAVVTGDCPVSVEKIVNIENGTSCPSLGGKPKLFFIOACGGEQKDHGFVEAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWHAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416
DB 361 SWYVETLDDIFEQWHAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416

RESULT 6
ABJ01224
ID ABJ01224 standard; protein; 416 AA.
AC ABJ01224;
XX
XX 18-SEP-2002 (first entry)
DE Human caspase-9 SEQ ID NO: 30.
XX
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
KW autoimmune disease; cytostatic; immunosuppressive.
XX
XX Homo sapiens.
XX
XX US6376226-B1.
XX
XX 23-APR-2002.
XX
XX 26-APR-2000; 2000US-00561756.
XX
XX 09-JAN-1998; 98US-0070897P.
XX
XX 08-JAN-1999; 99US-00227721.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-453146/48.
XX
XX N-PSDB; ABT03972.

PT New rev-caspases engineered to contain the small subunit fused in frame N
PT -terminal to the large subunit, which is in reverse order to the wild
XX type caspases, are useful to treat cancer and autoimmune diseases.
PS Disclosure; Fig 19; 81pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
CC can be used in the gene therapy of cancer and autoimmune diseases. The
CC present sequence is a protein described in the exemplification of the
CC invention
XX
XX Sequence 416 AA;

Query Match 98.9%; Score 2157; DB 5; Length 416;
Best Local Similarity 99.0%; Pred. No. 2.6e-217;

Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRRLRLVEELQDQVLDVILSRELFPRPHMIEDIQRAGSGRRDQARQLII 60
DB 1 MDEADRLRLRRLRLVEELQDQVLDVILSRELFPRPHMIEDIQRAGSGRRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGKLSKPTLENLTPVILRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGKLSKPTLENLTPVILRPEIRKPEV 120
QY 121 LRPTPRVDITGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLLIINNWFRCRESGLRTR 180
DB 121 LRPTPRVDITGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLLIINNWFRCRESGLRTR 180
QY 181 TGSNIDCEKLRFRSSLSHFVVEVKGDLTAKMWLALLELARQDHGALDCCVVWILSHGCQ 240
DB 181 TGSNIDCEKLRFRSSLSHFVVEVKGDLTAKMWLALLELARQDHGALDCCVVWILSHGCQ 240
QY 241 ASHLQFPFCAVVTGDCPVSVEKIVNIENGTSCPSLGGKPKLFFIOACGGEQKDHGFVEAS 300
DB 241 ASHLQFPFCAVVTGDCPVSVEKIVNIENGTSCPSLGGKPKLFFIOACGGEQKDHGFVEAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWHAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416
DB 361 SWYVETLDDIFEQWHAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416

RESULT 7
AAG67375
ID AAG67375 standard; protein; 416 AA.
XX
XX AAG67375;
AC
XX 13-NOV-2001 (first entry)
DT
XX
XX Amino acid sequence of human Mch6 polypeptide.
DE
XX
XX Mch6; ced-3 homologue; ICE; interleukin-1-beta converting enzyme;
KW aspartate-specific cysteine protease; ASCP; apoptotic cell death;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW retinitis pigmentosa; cerebellar degeneration; myelodysplastic syndrome;
KW aplastic anemia; ischemic injury; myocardial infarction; stroke; cancer;
KW reperfusion injury; autoimmune disease; systemic lupus erythematosus;
KW immune-mediated glomerulonephritis; viral infection; cell death.
XX
XX Homo sapiens.
XX
XX US6274318-B1.
XX
XX 14-AUG-2001.
XX
XX 13-MAY-1999; 99US-00311760.
XX
XX 29-MAY-1997; 97US-00865579.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
PI
XX
XX WPI; 2001-540372/60.
XX
XX N-PSDB; AAH77927.

PT Identifying mammalian homolog ced-3 homolog (Mch) 6 activity modulators,
PT useful for treating lymphomas, carcinomas and hormone dependent tumors,
PT Alzheimer's disease, Parkinson's disease, comprises using Mch6
PT polypeptide.
XX
XX Example 1; Fig 1a-c; 36pp; English.
PS
XX

CC The present sequence represents a human Mch6 polypeptide. Mch6 is a ced-3
CC homologue, and is a member of the ICE (interleukin-1-beta converting
CC enzyme) family of aspartate-specific cysteine proteases (ASCPs). The
CC specification describes a method for identifying mammalian Mch6 activity
CC modulators (inhibitors or enhancers). The compounds identified by the
CC method are useful as pharmaceuticals for treating or preventing diseases
CC characterized by increased apoptotic cell death such as Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
CC pigmentosa, or cerebellar degeneration, myelodysplastic syndromes such as
CC aplastic anemia, ischemic injury including myocardial infarction, stroke
CC and reperfusion injury. The compounds are also useful for treating
CC diseases characterized by loss of apoptotic cell death such as cancers,
CC e.g. lymphomas, carcinomas and hormone dependent tumours such as breast,
CC prostate and ovarian cancer. Increased cell survival or apoptosis
CC inhibition also results in autoimmune diseases such as systemic lupus
CC erythematosus and immune-mediated glomerulonephritis as well as viral
CC infections such as herpes virus, pox virus and adenovirus and the novel
CC identified compounds are useful for treating these conditions. The Mch6
CC inhibitors are used to treat or to reduce severity of diseases
CC characterized by increased programmed cell death
XX
SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217; Indels 0; Gaps 0;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRLFRPHMIEDIQAGSGRRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLWDALLSELFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGCHLIINNVCRESGLRTR 180
DB 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGCHLIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRFRSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVILSHGQC 240
DB 181 TGSNIDCEKLRFRSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVILSHGQC 240
QY 241 ASHLQFPAGVYTGDCPVSVKIVNIFNGTSCPSLGGPKLFFIOACGGEQKHDFEVS 300
DB 241 ASHLQFPAGVYTGDCPVSVKIVNIFNGTSCPSLGGPKLFFIOACGGEQKHDFEVS 300
QY 301 TSPDESQSNPEPDATPQEGRLTFDQDLDAISSLPTPSDIFVSYSTFFGVSWRDPKSG 360
DB 301 TSPDESQSNPEPDATPQEGRLTFDQDLDAISSLPTPSDIFVSYSTFFGVSWRDPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416

RESULT 8
AAU08315
ID AAU08315 standard; protein; 416 AA.
XX AAU08315;
XX
DT 04-DEC-2001 (first entry)
XX Human aspartate-specific cysteine protease, MCH6.
XX Human; aspartate-specific cysteine protease; MCH6; neurotropic;
XX neuroprotective; anti-Parkinsonian; antianemic; vasotropic; cardiant;
XX cerebroprotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
XX Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
XX cerebellar degeneration; myelodysplastic syndrome; aplastic anemia;
XX ischaemic injury; myocardial infarction; stroke; reperfusion injury;
XX amyotrophic lateral sclerosis.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Active-site 285..289
FT Cleavage-site 312..316
FT /label= Granzyme beta cleavage site
FT /note= "Cleavage occurs after Asp at position 315"
FT Cleavage-site 327..331
FT /label= Granzyme beta cleavage site
FT /note= "Cleavage occurs after Asp at position 330"
XX
PN US2001016345-A1.
XX
XX 23-AUG-2001.
XX
XX 22-DEC-2000; 2000US-00746731.
XX
XX 29-MAY-1997; 97US-00865579.
XX
XX 25-FEB-1999; 99US-00257218.
XX
XX (ALNE/) ALNEMRI E S.
XX (FERN/) FERNANDES-ALNEMRI T.
XX (LITW/) LITWACK G.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX
XX WPI; 2001-535542/59.
XX N-PSDB; AAS12629.
XX
XX New Mch6 polypeptides and genes encoding the polypeptides useful for
XX diagnosing, treating or reducing the severity of cell death-mediated
XX diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
XX Parkinson's disease.
XX
XX Claim 8; Fig 1; 15pp; English.
XX
XX The invention relates to an isolated gene encoding MCH6 (mammalian ced-3
XX homologue 6) an aspartate-specific cysteine protease and the MCH6
XX polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
XX to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
XX death-mediated diseases (i.e. apoptotic) such as neurodegenerative
XX diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
XX lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
XX myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
XX myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
XX nucleic acids and polypeptides can also be used to diagnose or generate
XX reagents to diagnose diseases mediated or characterised by programmed
XX cell death. A purified recombinant MCH6 protein can be used to measure
XX hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
XX a continuous fluorometric assay. The present sequence represents human
XX MCH6
XX
XX Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRLFRPHMIEDIQAGSGRRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLWDALLSELFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGCHLIINNVCRESGLRTR 180
DB 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGCHLIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRFRSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVILSHGQC 240

Db 181 TGSNIDCEKLRFRFSSPHFMVEVKGDLTAKMWLALLELAQDGHGALDCCVVVILSHGCG 240
 QY 241 ASHLQFPQAVYGTGDCPVSVKIVNIENGTSCLPSLGGKPKLFFIQACGGKQKHGFVEAS 300
 Db 241 ASHLQFPQAVYGTGDCPVSVKIVNIENGTSCLPSLGGKPKLFFIQACGGKQKHGFVEAS 300
 QY 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPTSPDIFVSVSTPFGFVSWRDPKSG 360
 Db 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPTSPDIFVSVSTPFGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 9

AAE08938
 ID AAE08938 standard; protein; 416 AA.

AC AAE08938;

XX 15-NOV-2001 (first entry)

DE Mammalian ced-3 homologue 6 (Mch6).

XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
 KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
 KW viral infection; cell death-mediated disease; neuroprotective.

XX Unidentified.

FF Key Location/Qualifiers
 FT Active-site 285..290 /note= "Active site pentapeptide"
 FT Cleavage-site 315..316
 FT Cleavage-site 330..331

XX US6271361-B1.

XX 07-AUG-2001.

PF 25-FEB-1999; 99US-00257218.

XX 29-MAY-1997; 97US-00865579.

XX (UYJE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Fernandes-Alnemri T, Litwack G;

DR WPI; 2001-528686/58.

XX N-PSDB; AAD15656.

XX New apoptotic genes and their apoptotic protease products, useful for
 PT modulating apoptosis for the therapeutic treatment of human diseases,
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
 PT disease.

PS Claim 2; Fig 1; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease,
 CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
 CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
 CC are useful for modulating apoptosis for the therapeutic treatment of
 CC human diseases. Mch6 sequences are useful for upregulating apoptosis
 CC (e.g. for treating cancers, autoimmune disease or viral infections) or
 CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
 CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
 CC useful for diagnosing, treating or reducing the severity of cell death-
 CC mediated diseases, as well as other diseases mediated by either increased
 CC or decreased programmed cell death. The present amino acid sequence is
 CC Mch6

XX SQ

Sequence 416 AA;

Query Match

Best Local Similarity 98.8%; Score 2153; DB 4; Length 416;

Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDQWVLLSRLFRPHMIEDIORAGSGSRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEELQVDQDQWVLLSRLFRPHMIEDIORAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFTISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVWLRPEIRKPEV 120

Db 61 DLETRGSQALPLFTISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVWLRPEIRKPEV 120

QY 121 LRPEPRPVDIGGGGFGVGALESRLGNADLAYILSMPEPGHCLIIINNVPFCRESGLRTR 180

Db 121 LRPEPRPVDIGGGGFGVGALESRLGNADLAYILSMPEPGHCLIIINNVPFCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSSPHFMVEVKGDLTAKMWLALLELAQDGHGALDCCVVVILSHGCG 240

Db 181 TGSNIDCEKLRFRFSSPHFMVEVKGDLTAKMWLALLELAQDGHGALDCCVVVILSHGCG 240

QY 241 ASHLQFPQAVYGTGDCPVSVKIVNIENGTSCLPSLGGKPKLFFIQACGGKQKHGFVEAS 300

Db 241 ASHLQFPQAVYGTGDCPVSVKIVNIENGTSCLPSLGGKPKLFFIQACGGKQKHGFVEAS 300

QY 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPTSPDIFVSVSTPFGFVSWRDPKSG 360

Db 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPTSPDIFVSVSTPFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

Db 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 10

AAE84374

ID AAE84374 standard; protein; 416 AA.

AC AAE84374;

DT 22-AUG-2001 (first entry)

DE Amino acid sequence of aspartate-specific cysteine protease Mch6.

KW Human; apoptotic protease; Mch6; aspartate-specific cysteine protease;
 KW cell death; cancer; autoimmune disease; systemic lupus erythematosus;
 KW viral infection; degenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; myelodysplastic syndrome; myocardial infarction;
 KW stroke.

OS Homo sapiens.

XX US2001006779-Al.

XX 05-JUL-2001.

PF 29-MAY-1997; 97US-00865579.

XX 29-MAY-1997; 97US-00865579.

XX (ALNE/) ALNEMRI E S.

PA (FERN/) FERNANDES-ALNEMRI T.

XX (LITW/) LITWACK G.

PI Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX WPI; 2001-389294/41.

XX N-PSDB; AAE25191.

XX Isolated gene encoding a human apoptotic protease known as Mch6, useful
 PT in the diagnosis or treatment of cell death-mediated conditions, e.g.

PT cancers and autoimmune diseases such as systemic lupus erythematosus.

XX Claim 8; Fig 1A-C; 15pp; English.

XX The present sequence represents a human apoptotic protease, designated
XX Mch6. Mch6 is an aspartate-specific cysteine protease. Mch6 polypeptides
XX and polynucleotides can be used to diagnose, treat or reduce the severity
XX of cell death-mediated conditions, e.g. cancers, autoimmune diseases such
XX as systemic lupus erythematosus, viral infections such as herpesvirus,
XX degenerative disorders such as Alzheimer's disease and Parkinson's
XX disease, myelodysplastic syndromes such as myocardial infarction and
XX stroke. They can also be used to screen for compounds that inhibit or
XX promote Mch6 mediated apoptosis

XX SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKQWVLLALLELARDQDHALDCCVVLISHGCG 240
Db 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKQWVLLALLELARDQDHALDCCVVLISHGCG 240
Qy 241 ASHLQFPGAVYGTDCGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTDCGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKDHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTSDIFVSYSTPFGFVSWRDPKSG 360
Qy 361 SWYVETLDDIFEQWAHSEDQLSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDQLSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 11
ABB82738 standard; protein; 416 AA.

XX ABB82738;
XX AC ABB82738;
XX 07-MAR-2003 (first entry)
XX Human caspase-9 polypeptide.
XX Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human.
XX Homo sapiens.
XX WO200290931-A2.
XX 14-NOV-2002.
XX 07-MAY-2002; 2002WO-US014487.
XX 07-MAY-2001; 2001US-0289223P.
XX 12-FEB-2002; 2002US-0356934P.
XX (BURN-) BURNHAM INST.

XX Reed JC;

XX WPI; 2003-111999/10.

XX Determining a prognosis for survival for a cancer patient, useful for
XX PT determining if the patient is at risk for relapse, comprises measuring a
XX PT level of TUCAN in a sample from the patient, and comparing it to a
XX PT reference level.

XX Example; Page 125-126; 153pp; English.

XX The invention relates to determining a prognosis for survival for a
XX cancer patient. The method involves (a) measuring a level of a tumour up-
XX regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
XX cell-containing sample from the cancer patient; and (b) comparing the
XX level of TUCAN in the sample to a reference level of TUCAN, where a low
XX level of TUCAN in the sample correlates with increased survival of the
XX patient. Alternatively, the method involves measuring levels of TUCAN and
XX one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
XX Smac in a neoplastic cell-containing sample from the cancer patient. The
XX method is useful for determining if the patient is at risk for relapse,
XX or for determining a proper course of treatment for a patient with
XX cancer. The method is also useful for monitoring the effectiveness of a
XX course of treatment for a patient with cancer, e.g. colon cancer,
XX gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
XX leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
XX present sequence represents a human caspase-9 polypeptide

XX SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 6; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKQWVLLALLELARDQDHALDCCVVLISHGCG 240
Db 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKQWVLLALLELARDQDHALDCCVVLISHGCG 240
Qy 241 ASHLQFPGAVYGTDCGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTDCGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKDHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTSDIFVSYSTPFGFVSWRDPKSG 360
Qy 361 SWYVETLDDIFEQWAHSEDQLSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDQLSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 12
ADE52020 standard; protein; 416 AA.

XX ADE52020;
XX AC ADE52020;
XX 29-JAN-2004 (first entry)
XX Human mammalian ced-3 homologue 6 (Mch6).

XX cytostatic; virucide; nootropic; neuroprotective; antiparkinsonian;
 KW cardiant; apoptosis modulator; aspartate-specific cysteine protease;
 KW gene therapy; aspartate-specific cysteine protease agonist;
 KW aspartate-specific cysteine protease antagonist; Mch6;
 KW mammalian ced-3 homologue 6; apoptosis; cancer; viral infection;
 KW degenerative disorder; Alzheimers disease; Parkinsons disease;
 KW myocardial infarction; human; mammalian ced-3 homologue 6; Mch6.
 XX
 OS Homo sapiens.
 XX
 XX US2002183504-A1.
 XX
 XX 05-DEC-2002.
 XX
 XX 29-JAN-2002; 2002US-00059749.
 XX
 XX 29-MAY-1997; 97US-00865579.
 XX
 XX 25-FEB-1999; 99US-00257218.
 XX
 XX 22-DEC-2000; 2000US-00746731.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX
 XX WPI; 2004-040943/04.
 XX
 XX New isolated gene encoding a mammalian ced-3 homologue 6, for modulating
 PT apoptosis for the therapeutic treatment of human diseases, such as
 PT cancers and degenerative disorders.
 XX
 XX Claim 8; SEQ ID NO 2; 15pp; English.
 XX
 XX The invention describes an isolated gene (I) encoding Mch6 (mammalian ced
 CC -3 homologue 6), or a functional fragment of it. (I) And the polypeptide
 CC encoded by (i) is used to modulate apoptosis for the therapeutic
 CC treatment of human diseases. (I) Is used to prepared a recombinant
 CC aspartate-specific cysteine protease, that it encodes. The recombinant
 CC protease can be used to screen for Mch6 inhibitors. Disorders involving
 CC apoptosis that can be diagnosed or treated by (I) or the polypeptide it
 CC encodes, including cancers, viral infections, degenerative disorders,
 CC such as Alzheimers and Parkinsons disease, and myocardial infarction.
 CC This is the amino acid sequence of human mammalian ced-3 homologue 6
 CC (Mch6), a member of the aspartate-specific cysteine protease (ASCP)
 CC family of proteases.
 XX
 XX Sequence 416 AA;
 SQ

Query Match
 Best Local Similarity 98.8%; Score 2153; DB 8; Length 416;
 Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLMDVLLSRLFLPHMEDIQAGSGSRDQARQLII 60
 DB 1 MDEADRLRLRCRLRLVEQLVDQLMDVLLSRLFLPHMEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLETGTGDMLASFLTRNRQAKLSKPTLENLTPVLRPEIRKPKV 120
 DB 61 DLETRGSQALPLFISCLETGTGDMLASFLTRNRQAKLSKPTLENLTPVLRPEIRKPKV 120

QY 121 LRPEPRPVDIGSGGFDVGALESRLGNADLAVILSMPECGHCLINNVNFCRESGLRTR 180
 DB 121 LRPEPRPVDIGSGGFDVGALESRLGNADLAVILSMPECGHCLINNVNFCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSLHFMVVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQQ 240
 DB 181 TGSNIDCEKLRFRFSSPHFMVVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQQ 240

QY 241 ASHLOPFGAVYGTDCGVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGEQKDHGFVAS 300
 DB 241 ASHLOPFGAVYGTDCGVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGEQKDHGFVAS 300

QY 301 TSPFESPGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWEDPKSG 360

DB 301 TSPFESPGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWEDPKSG 360
 QY 361 SWYVETLDDIFEWAHSEDLSILLRRVANAVSVGIYKQMGCCNFRLKLLFFKTS 416
 DB 361 SWYVETLDDIFEWAHSEDLSILLRRVANAVSVGIYKQMGCCNFRLKLLFFKTS 416

RESULT 13
 ADA10675
 ID ADA10675 standard; protein; 416 AA.
 XX
 AC ADA10675;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human caspase-9 protein D315A/D330A mutant.
 XX
 KW Human; caspase-9; anti-HIV; nootropic; neuroprotective; vasotropic;
 KW cytostatic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; muten.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 315 /note= "Wild-type Asp substituted by Ala"
 FT Misc-difference 330 /note= "Wild-type Asp substituted by Ala"
 FT
 XX US2002160975-A1.
 XX
 XX 31-OCT-2002.
 XX
 XX 06-FEB-2002; 2002US-00068569.
 XX
 XX 08-FEB-2001; 2001US-0267966P.
 XX
 XX 24-AUG-2001; 2001US-00939293.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Alnemri ES;
 XX
 XX WPI; 2003-219992/21.
 XX
 XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.
 XX
 XX Claim 37; Page; 52pp; English.
 XX

The invention relates to an isolated nucleic acid molecule comprising a
 polynucleotide that encodes a polypeptide or peptide, or its variants
 that specifically binds to at least a portion of an inhibitor of
 apoptosis protein (IAP). Also included are a peptide or a polypeptide
 comprising at least an N terminus sequence of caspase-9 N-terminal
 linker sequence, a first portion of an IAP and a second portion of a
 containing a mutated active site, where the peptide or polypeptide
 specifically binds at least a portion of an IAP and lacks cysteine
 protease activity, and at least a portion of caspase-3, where the peptide
 or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 procaspase-9, which fails to undergo normal processing and possesses wild
 type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 expression vector comprising any of the nucleic acids, a host cell
 containing the expression vector, an antibody that specifically binds to
 the peptide or polypeptide, an antibody that specifically binds to an

CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.
XX
XX
XX Sequence 416 AA;

Query Match 98.6%; Score 2150; DB 6; Length 416;
Best Local Similarity 98.8%; Pred. No. 1.4e-216;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETPRVDITGSGFGFVGVGALSRLGNADLAYILSMFPCGHCLILNNVFCRESGLRTR 180
DB 121 LRPETPRVDITGSGFGFVGVGALSRLGNADLAYILSMFPCGHCLILNNVFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSLHFMVEVKGDLTAKKMWLALLEARQDHGALDCCVVLISHGQC 240
DB 181 TGSNIDCEKLRRLRRFSLHFMVEVKGDLTAKKMWLALLEARQDHGALDCCVVLISHGQC 240
QY 241 ASHLQFPAGVGTDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKHDFEVS 300
DB 241 ASHLQFPAGVGTDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKHDFEVS 300
QY 301 TSPDESFGSNPEPATPFQGLRTFDQDLAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPATPFQGLRTFDQDLAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLRLRVANAVSVKGIYQMPGCFNLRKLPFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLQSLRLRVANAVSVKGIYQMPGCFNLRKLPFKTS 416

RESULT 14
ADA10676
ID ADA10676 standard; protein; 416 AA.

XX ADA10676;

XX 06-NOV-2003 (first entry)

DE Human caspase-9 protein E306A/D315A/D330A mutant.

XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
XX cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
XX caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
XX Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
XX ischaemic injury; cancer; autoimmune disease; mutant; mutin.

OS Synthetic.
OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 306

FT /note= "Wild-type Glu substituted by Ala"

FT Misc-difference 315

FT /note= "Wild-type Asp substituted by Ala"
FT Misc-difference 330
XX /note= "Wild-type Asp substituted by Ala"
PN US2002160975-A1.
XX 31-OCT-2002.
XX 06-FEB-2002; 2002US-00068569.
XX 08-FEB-2001; 2001US-0267966P.
XX 24-AUG-2001; 2001US-00939293.
XX (UJJE-) UNIV JEFFERSON THOMAS.
XX Alnemri ES;
XX WPI; 2003-219992/21.
XX New nucleic acid molecules encoding a peptide or polypeptide that binds
XX to a portion of an inhibitor of apoptosis protein, useful for inducing
XX apoptosis and identifying inhibitors or enhancers of apoptosis for
XX treating AIDS, or cancer.
XX Claim 38; Page; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX (comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically
XX binds at least a portion of an IAP and a second portion of a procaspase-9
XX containing a mutated active site, where the peptide or polypeptide
XX specifically binds at least a portion of an IAP and lacks cysteine
XX protease activity, and at least a portion of caspase-3, where the peptide
XX or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
XX an IAP or an IAP Bir3 domain) or at least a portion of a mutated
XX procaspase-9, which fails to undergo normal processing and possesses wild
XX type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
XX polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
XX expression vector comprising any of the nucleic acids, a host cell
XX containing the expression vector, an antibody that specifically binds to an
XX the peptide or polypeptide, an antibody that specifically binds to an
XX epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
XX in a cell or stimulating apoptosis in a neoplastic or tumour cell,
XX identifying an inhibitor or enhancer of caspase-mediated apoptosis,
XX producing a compound that inhibits the peptide or polypeptide,
XX a process for the manufacture of a compound for inhibiting or enhancing
XX apoptosis in a cell. The nucleic acid molecules and peptides or
XX polypeptides are useful for inducing apoptosis and identifying inhibitors
XX or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
XX ischaemic injury, cancer, autoimmune diseases. The present sequence
XX represents the caspase-9 protein mutated to ablate the autocatalytic
XX cleavage site in the linker region. Note: the present sequence is not
XX shown in the specification but was created by the indexer using the
XX information in the claims and the wild type caspase-9 sequence.

XX Sequence 416 AA;

Query Match 98.3%; Score 2144; DB 6; Length 416;
Best Local Similarity 98.6%; Pred. No. 6.1e-216;
Matches 410; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120

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QY 121 LRPETPRVDIGSGGFDVGALSLRGNADLAYILSMPEPCGHCLIIINNVMFCRESGLRTR 180
Db |||||
QY 121 LRPETPRVDIGSGGFDVGALSLRGNADLAYILSMPEPCGHCLIIINNVMFCRESGLRTR 180
Db |||||
QY 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELALRQDHGALDCCVVILSHGCO 240
Db |||||
QY 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELALRQDHGALDCCVVILSHGCO 240
Db |||||
QY 241 ASHLQFPGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFTAQCGGQKHGFVEAS 300
Db |||||
QY 241 ASHLQFPGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFTAQCGGQKHGFVEAS 300
Db |||||
QY 301 TSPEDSPGNSNPEPATPFQEGRLTFQDLDAISLPTSPDIFVSYSTFPFGVSWRDPKSG 360
Db |||||
QY 301 TSPEDSPGNSNPEPATPFQEGRLTFQDLDAISLPTSPDIFVSYSTFPFGVSWRDPKSG 360
Db |||||
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db |||||
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db |||||
```

RESULT 15

ADAL0677
ID ADAL0677 standard; protein; 401 AA.

XX AC ADAL0677;

XX DT 06-NOV-2003 (first entry)

XX DE Human caspase-9 protein del316-330 mutant.

XX KW Human; caspase-9; anti-HIV; nootropic; neuroprotective; vasotropic;
KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
KW ischaemic injury; cancer; autoimmune disease; mutant; muten.

XX OS Synthetic.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Misc-difference 315..316
XX FT /note= "Residues 316-330 of the wild-type protein have
XX been deleted"

XX PN US2002160975-A1.
XX PD 31-OCT-2002.
XX PF 06-FEB-2002; 2002US-00068569.
XX PR 08-FEB-2001; 2001US-0267966P.
XX PR 24-AUG-2001; 2001US-00939293.

XX XX (UYJE-) UNIV JEFFERSON THOMAS.
XX PA Alnemri ES;
XX PI WPI; 2003-219992/21.
XX DR WPI; 2003-219992/21.
XX XX

XX FT New nucleic acid molecules encoding a peptide or polypeptide that binds
XX to a portion of an inhibitor of apoptosis protein, useful for inducing
XX apoptosis and identifying inhibitors or enhancers of apoptosis for
XX treating AIDS, or cancer.
XX PS Claim 39; Page: 52pp; English.

XX CC The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX (comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically

CC binds at least a portion of an IAP and a second portion of a procaspase-9
CC containing a mutated active site, where the peptide or polypeptide
CC specifically binds at least a portion of an IAP and lacks cysteine
CC protease activity, and at least a portion of caspase-3, where the peptide
CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
CC procaspase-9, which fails to undergo normal processing and possesses wild
CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
CC polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
CC expression vector comprising any of the nucleic acids, a host cell
CC containing the expression vector, an antibody that specifically binds to
CC the peptide or polypeptide, an antibody that specifically binds to an
CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumor cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.

XX SQ Sequence 401 AA;

Query Match 94.9%; Score 2069.5; DB 6; Length 401;
Best Local Similarity 95.7%; Pred. No. 3.9e-208;
Matches 398; Conservative 1; Mismatches 2; Indels 15; Gaps 1;
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QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGLSKPTLENTLPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGLSKPTLENTLPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFDVGALSLRGNADLAYILSMPEPCGHCLIIINNVMFCRESGLRTR 180
Db 121 LRPETPRVDIGSGGFDVGALSLRGNADLAYILSMPEPCGHCLIIINNVMFCRESGLRTR 180
QY 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELALRQDHGALDCCVVILSHGCO 240
Db 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELALRQDHGALDCCVVILSHGCO 240
QY 241 ASHLQFPGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFTAQCGGQKHGFVEAS 300
Db 241 ASHLQFPGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFTAQCGGQKHGFVEAS 300
QY 301 TSPEDSPGNSNPEPATPFQEGRLTFQDLDAISLPTSPDIFVSYSTFPFGVSWRDPKSG 360
Db 301 TSPEDSPGNSNPEPATPFQEGRLTFQDLDAISLPTSPDIFVSYSTFPFGVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 401

Search completed: August 3, 2004, 08:53:23
Job time : 57 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2004, 08:54:46 ; Search time 45 Seconds
(without alignments)
2899.824 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCFNLRKLFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2166	99.4	416	13	US-10-068-569-1	Sequence 1, Appli
2	2157	98.9	416	9	US-09-954-697-30	Sequence 30, Appl
3	2153	98.8	416	10	US-09-851-873-102	Sequence 102, App
4	2153	98.8	416	12	US-09-746-731-2	Sequence 2, Appli
5	2153	98.8	416	13	US-10-059-749-2	Sequence 4, Appli
6	2153	98.8	416	14	US-10-141-618-4	Sequence 4, Appli
7	1282	58.8	266	15	US-10-116-275-172	Sequence 172, App
8	773	35.5	159	12	US-10-424-599-174531	Sequence 174531,
9	468	21.5	93	13	US-10-014-269-27	Sequence 27, Appl
10	468	21.5	93	13	US-10-002-974-27	Sequence 27, Appl
11	468	21.5	93	14	US-10-314-506-27	Sequence 27, Appl
12	419	19.2	277	15	US-10-155-567-4	Sequence 4, Appli
13	418	19.2	264	13	US-10-103-448-3	Sequence 3, Appli
14	418	19.2	264	13	US-10-108-929-3	Sequence 3, Appli
15	418	19.2	277	9	US-09-895-263-4	Sequence 4, Appli

16	418	19.2	277	9	US-09-954-697-12	Sequence 12, Appl
17	418	19.2	277	10	US-09-851-873-98	Sequence 98, Appl
18	418	19.2	277	12	US-10-232-884-4	Sequence 4, Appli
19	418	19.2	277	14	US-10-214-932-108	Sequence 108, App
20	418	19.2	277	14	US-10-207-655-202	Sequence 202, App
21	418	19.2	277	14	US-10-280-670-5	Sequence 5, Appli
22	418	19.2	277	15	US-10-368-438-30	Sequence 30, Appl
23	418	19.2	277	16	US-10-408-765A-172	Sequence 172, App
24	418	19.2	277	16	US-10-701-490-11	Sequence 11, Appl
25	414	19.0	452	14	US-10-205-219-52	Sequence 52, Appl
26	409.5	18.8	284	12	US-10-232-884-5	Sequence 5, Appli
27	409.5	18.8	451	9	US-09-888-243-28	Sequence 28, Appl
28	409	18.8	421	15	US-10-368-438-10	Sequence 10, Appl
29	409	18.8	435	8	US-08-459-455-51	Sequence 51, Appl
30	409	18.8	435	9	US-09-954-697-9	Sequence 9, Appli
31	409	18.8	435	10	US-09-851-873-97	Sequence 97, Appl
32	409	18.8	435	14	US-10-280-670-9	Sequence 9, Appli
33	409	18.8	441	8	US-08-459-455-43	Sequence 43, Appl
34	401.5	18.4	505	9	US-09-888-243-5	Sequence 5, Appli
35	395.5	18.1	503	8	US-08-459-455-36	Sequence 36, Appl
36	395.5	18.1	503	14	US-10-123-529-8	Sequence 8, Appli
37	390.5	17.9	464	15	US-10-368-438-18	Sequence 18, Appl
38	385.5	17.7	503	8	US-08-459-455-2	Sequence 2, Appli
39	385.5	17.7	503	9	US-09-888-243-29	Sequence 29, Appl
40	385.5	17.7	503	14	US-10-280-670-10	Sequence 10, Appl
41	385	17.7	457	12	US-10-296-115-1281	Sequence 1281, Ap
42	383	17.6	479	9	US-09-410-194-20	Sequence 20, Appl
43	383	17.6	479	10	US-09-851-873-101	Sequence 101, App
44	383	17.6	479	15	US-10-368-438-7	Sequence 7, Appli
45	383	17.6	496	12	US-10-232-884-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-068-569-1
; Sequence 1, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-1

Query Match	99.4%	Score	2166	DB	13	Length	416
Best Local Similarity	99.3%	Pred. No.	1.2e-206				
Matches	413	Conservative	1	Mismatches	2	Indels	0
Gaps	0						
QY	1	MDEADRLRLRCRLRLVEELQVQDMVLLSRELFRPHMIEDIQAGSGRRDQARQLII	60				
Db	1	MDEADRLRLRCRLRLVEELQVQDMVLLSRELFRPHMIEDIQAGSGRRDQARQLII	60				
QY	61	DLETRGSQALPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV	120				
Db	61	DLETRGSQALPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV	120				
QY	121	LRPETPRVDIGSGFGDVGALSLRGNAIDLAYILSMPCGCHLIINNVCRESGLRTR	180				
Db	121	LRPETPRVDIGSGFGDVGALSLRGNAIDLAYILSMPCGCHLIINNVCRESGLRTR	180				
QY	181	TGSNIDCEKRRRFSLSHFVMEVKGDLTAKQWVLLALLELARQDRGALDCCVVVILSHGQ	240				

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QY 241 ASHLQFPFVAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGKQKHGFEVAS 300
;
Db 241 ASHLQFPFVAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGKQKHGFEVAS 300
;
QY 301 TSPDESFGNPNPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFFGVSWRDPKSG 360
;
Db 301 TSPDESFGNPNPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFFGVSWRDPKSG 360
;
QY 361 SWVYETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
;
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;

RESULT 2
US-09-954-697-30
; Sequence 30, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30

Query Match 98.9%; Score 2157; DB 9; Length 416;
Best Local Similarity 99.0%; Pred. No. 9.1e-206;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MDEADRLRLRCRLRLVEELQVDQIMVLLSRELFRPHMIEDIORAGSGRRDQARQLII 60
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RESULT 3
US-09-851-873-102
; Sequence 102, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
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; APPLICANT: Kietzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-102

Query Match 98.8%; Score 2153; DB 10; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db 121 LRPEPRPVDIGSGGFGDVGALESRLGNADLAYILSMPEPGHCLIIINNPNFCRESGLRTR 180
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Db 181 TGSNIDCEKLRRLRRFSSLHFVVEKGLDTAKKMWLALLELAQQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPFVAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGKQKHGFEVAS 300
Db 241 ASHLQFPFVAVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGKQKHGFEVAS 300
QY 301 TSPDESFGNPNPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFFGVSWRDPKSG 360
Db 301 TSPDESFGNPNPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFFGVSWRDPKSG 360
QY 361 SWVYETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
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RESULT 4
US-09-746-731-2
; Sequence 2, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
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; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-746-731-2

Query Match          98.8%; Score 2153; DB 12; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRRDQARQLII 60
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Db 61 DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
QY 121 LRPETPRPDVIGSGGFDVGALESFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 180
Db 121 LRPETPRPDVIGSGGFDVGALESFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 180
QY 181 TGSNIDCEKLRFRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
Db 181 TGSNIDCEKLRFRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 5
US-10-059-749-2
; Sequence 2, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match          98.8%; Score 2153; DB 13; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRRDQARQLII 60
QY 61 DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
Db 61 DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
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Db 121 LRPETPRPDVIGSGGFDVGALESFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 180
QY 181 TGSNIDCEKLRFRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
Db 181 TGSNIDCEKLRFRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
QY 301 TSPEDSPGSPNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFPGFVSWRDPKSG 360
Db 301 TSPEDSPGSPNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 6
US-10-141-618-4
; Sequence 4, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; TITLE OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
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; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-618-4

Query Match          98.8%; Score 2153; DB 14; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPTPRPVDIGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRRPFSSLFHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
Db 140 -----
QY 241 ASHLQFPVAVYGTGCPVSVKEKIVINFGTSCPSLGGKPKLFFIQACGGEOKDHGFVEAS 300
Db 140 -----EOKDHGFVEAS 150
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTFPFGFVSRDPKSG 360
Db 151 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTFPFGFVSRDPKSG 210
QY 361 SWYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKILFFKTS 416
Db 211 SWYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKILFFKTS 266

RESULT 7
US-10-116-275-172
; Sequence 172, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20067
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-172

Query Match          59.8%; Score 1282; DB 15; Length 266;
Best Local Similarity 63.2%; Pred. No. 7.1e-119;
Matches 263; Conservative 0; Mismatches 3; Indels 150; Gaps 1;
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QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 180
Db 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 180
QY 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPTPRPVDIGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGGFGDV----- 139
QY 181 TGSNIDCEKLRRRPFSSLFHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
Db 140 ----- 139
QY 241 ASHLQFPVAVYGTGCPVSVKEKIVINFGTSCPSLGGKPKLFFIQACGGEOKDHGFVEAS 300
Db 140 -----EOKDHGFVEAS 150
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTFPFGFVSRDPKSG 360
Db 151 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTFPFGFVSRDPKSG 210
QY 361 SWYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKILFFKTS 416
Db 211 SWYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKILFFKTS 266

RESULT 8
US-10-424-599-174531
; Sequence 174531, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174531
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12861C.1.pep
US-10-424-599-174531

Query Match          35.5%; Score 773; DB 12; Length 159;
Best Local Similarity 96.9%; Pred. No. 1.7e-68;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
Db 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
QY 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPTPRPVDIGSGGFGDVGALSLRGNADLAYILSMPE 159
Db 121 LRPTPRPVDIGSGGFGDVGASESLRGNAYLAYILSMPE 159

RESULT 9
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
```

; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT APPLICATION NUMBER: US/10/014,269
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27

Query Match 21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 10

US-10-002-974-27
; Sequence 27, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan I.
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-974-27

Query Match 21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 11

US-10-314-506-27
; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori

; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,269
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,289
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-506-27

Query Match 21.5%; Score 468; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 12

US-10-155-567-4
; Sequence 4, Application US/10155567
; Publication No. US20030219421A1
; GENERAL INFORMATION:
; APPLICANT: CHRISTAKOS, Sylvia
; TITLE OF INVENTION: CALBINDIN-D 28K PROTECTION AGAINST GLUCOCORTICOID INDUCED CELL DEATH
; FILE REFERENCE: 267/266
; CURRENT APPLICATION NUMBER: US/10/155,567
; CURRENT FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 277
; TYPE: PRT
; ORGANISM: homosapiens
US-10-155-567-4

Query Match 19.2%; Score 419; DB 15; Length 277;
Best Local Similarity 33.2%; Pred. No. 7.4e-33;
Matches 91; Conservative 50; Mismatches 91; Indels 42; Gaps 4;

QY 150 DLAYILSMPEPCGHCILINNVNFCRSGLETRTGSNIDCEKLRRRFSSLIHPMVEVKGDLTA 209
Db 34 DTGYKMDYPENGLCIIINNNKFNHKTGMTSGTDVDAANLRETFRNLKYEVRNKNDLTR 93

QY 210 KKMVLALLELRQDHGALDCCVVVILSHGCOASHLQFPGCAVYGTDCGPVSVKIVNIENS 269
Db 94 EEIVELMRDVSKEHSHKRSFVCVLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145

QY 270 TSCPSLGGKPKLFFFTQACGGEQKHGFVASTSPDESFGSNPEPDATPFQGLRTFDQL 329
Db 146 DRCRSLTGKPKLFIQACRGTELDGCIETDSQVDDM----- 182

QY 330 DAISLPLTPSDIFVSYSTFPGFVSWRDPKSGWYVETLLDDIFEQWHSDDLQSLLRVAN 389
Db 183 -ACHKIPVDADFLYAISTAPGYISWNSKSGSWFTQSLCAMLKQYADKLEFMHILTRVNR 241

QY 390 AVSVK-----GIYKQMPGCFNFKKLFF 413
Db 242 KVATEFESFSPDATHAKKQIPCIVSMITKELYF 275

RESULT 13

US-10-103-448-3
; Sequence 3, Application US/10103448
; Publication No. US20020155579A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Wu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D1
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-103-448-3

Query Match 19.2%; Score 418; DB 13; Length 264;
Best Local Similarity 33.2%; Pred. No. 8.6e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMFPCGCHLIINNUNFCRESGLRTRTGSNIDCEKLRFRFSSLFHFMVEVKDGLTA 209
Db 21 DNSYKMDYPENGLCIIINNKNFKSTGTSRSGTSDVDAAANLRETFRNKLYEVRNKNDLTR 80
QY 210 KKVVLALLELARDHGDALDCCVVVILSHGCOASHLQFPFAGVYGTGDCPVSVEKIVNIFNG 269
Db 81 EEIVELMRDVSKEHSHKRSFVCLVSHGEE-----GIIFGTNG-FVDLKKITNFRPG 132
QY 270 TSCPSLGGKPKLFFIQACGGQKHGFEVASTSPDESFGSNPEPDATPFQEGRLTFDQL 329
Db 133 DRCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 169
QY 330 DAISLPTPSDIFVSYSTFGFVSWRDPKSGSWVETLDDIFEQWASEDLQSLLLRVAN 389
Db 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDSGFWFIQSLCAMLKQYADKLEFPHMLTRVNR 228
QY 390 AVSVK-----GIYKMPGCGFNFLRKKLFF 413
Db 229 KVATEFESFSDATFHAKKQIPCIVSMLTKEYLF 262

RESULT 14
US-10-108-929-3
; Sequence 3, Application US/10108929
; Publication No. US20020197702A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Wu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D2
; CURRENT APPLICATION NUMBER: US/10/108,929
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-108-929-3

Query Match 19.2%; Score 418; DB 13; Length 264;
Best Local Similarity 33.2%; Pred. No. 8.6e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMFPCGCHLIINNUNFCRESGLRTRTGSNIDCEKLRFRFSSLFHFMVEVKDGLTA 209

Db 21 DNSYKMDYPENGLCIIINNKNFKSTGTSRSGTSDVDAAANLRETFRNKLYEVRNKNDLTR 80
QY 210 KKVVLALLELARDHGDALDCCVVVILSHGCOASHLQFPFAGVYGTGDCPVSVEKIVNIFNG 269
Db 81 EEIVELMRDVSKEHSHKRSFVCLVSHGEE-----GIIFGTNG-FVDLKKITNFRPG 132
QY 270 TSCPSLGGKPKLFFIQACGGQKHGFEVASTSPDESFGSNPEPDATPFQEGRLTFDQL 329
Db 133 DRCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 169
QY 330 DAISLPTPSDIFVSYSTFGFVSWRDPKSGSWVETLDDIFEQWASEDLQSLLLRVAN 389
Db 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDSGFWFIQSLCAMLKQYADKLEFPHMLTRVNR 228
QY 390 AVSVK-----GIYKMPGCGFNFLRKKLFF 413
Db 229 KVATEFESFSDATFHAKKQIPCIVSMLTKEYLF 262

RESULT 15
US-09-895-263-4
; Sequence 4, Application US/09895263
; Patent No. US20020076793A1
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,263
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-251-6015
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-895-263-4

Query Match 19.2%; Score 418; DB 9; Length 277;
Best Local Similarity 33.2%; Pred. No. 9.3e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMFPCGCHLIINNUNFCRESGLRTRTGSNIDCEKLRFRFSSLFHFMVEVKDGLTA 209
Db 34 DNSYKMDYPENGLCIIINNKNFKSTGTSRSGTSDVDAAANLRETFRNKLYEVRNKNDLTR 93

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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:20 ; Search time 19 Seconds
(without alignments)
1130.337 Million cell updates/sec

Title: US-09-961-201A-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRLVLEL.....YKQMPGCCFNLKXKLPFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
.listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	3	US-08-852-936C-1
2	2180	100.0	416	3	US-09-300-328-1
3	2180	100.0	416	4	US-09-069-023-23
4	2157	98.9	416	4	US-09-561-756-30
5	2157	98.9	416	4	US-09-227-721-30
6	2157	98.9	416	4	US-09-354-697-30
7	2153	98.8	416	3	US-09-257-218-2
8	2153	98.8	416	3	US-09-311-760-2
9	2153	98.8	416	4	US-08-865-579-2
10	2153	98.8	416	4	US-10-059-749-2
11	1083	49.7	203	3	US-08-852-936C-4
12	1083	49.7	203	3	US-09-300-328-4
13	418	19.2	277	3	US-08-591-605-2
14	418	19.2	277	3	US-08-964-308-6
15	418	19.2	277	3	US-08-462-969B-4
16	418	19.2	277	3	US-08-964-313-6
17	418	19.2	277	4	US-09-069-138-6
18	418	19.2	277	4	US-09-561-756-12
19	418	19.2	277	4	US-09-227-721-12
20	418	19.2	277	4	US-08-983-502-30
21	418	19.2	277	4	US-09-124-934A-4
22	418	19.2	277	4	US-08-724-378D-5
23	418	19.2	277	4	US-08-334-251D-4
24	418	19.2	277	4	US-09-516-747-30
25	418	19.2	277	4	US-09-954-697-12
26	418	19.2	277	5	PCT-US96-10521-30
27	417	19.1	277	4	US-09-291-289-11

28 409 18.8 277 2 US-08-890-542A-2
29 409 18.8 421 4 US-08-983-502-10
30 409 18.8 421 4 US-09-516-747-10
31 409 18.8 421 5 PCT-US96-10521-10
32 409 18.8 435 3 US-08-258-287B-53
33 409 18.8 435 3 US-08-368-704C-51
34 409 18.8 435 4 US-09-561-756-9
35 409 18.8 435 4 US-09-227-721-9
36 409 18.8 435 4 US-08-816-075-2
37 409 18.8 435 4 US-08-724-378D-9
38 409 18.8 435 4 US-09-954-697-9
39 409 18.8 441 3 US-08-258-287B-44
40 409 18.8 441 3 US-08-368-704C-43
41 408 18.7 277 3 US-08-964-308-10
42 408 18.7 277 3 US-08-964-313-10
43 408 18.7 277 4 US-09-069-138-10
44 405 18.6 435 5 PCT-US94-07127A-4
45 401.5 18.4 505 2 US-08-394-189B-5

ALIGNMENTS

RESULT 1
US-08-852-936C-1
; Sequence 1, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; NUMBER OF INVENTIONS: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936C
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Sequence 2, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 53, Appl
Sequence 51, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 44, Appl
Sequence 43, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 4, Appli
Sequence 5, Appli

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US-08-852-936C-1
Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQDQMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
Db 1 MDEADRLRLRCRLRLVEELQVDQDQMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
Qy 61 DLETRGSOALPLFISCLDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSOALPLFISCLDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Qy 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRLRRSSSLHFVMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRSSSLHFVMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
Qy 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQGLRTFDQDIAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQDIAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
Qy 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 2
US-09-300-328-1
; Sequence 1, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,328
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936
; FILING DATE: 08-MAY-1997
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-300-328-1
Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQDQMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
Db 1 MDEADRLRLRCRLRLVEELQVDQDQMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
Qy 61 DLETRGSOALPLFISCLDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSOALPLFISCLDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Qy 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRLRRSSSLHFVMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRSSSLHFVMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
Qy 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQGLRTFDQDIAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQDIAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
Qy 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 3
US-09-069-023-23
; Sequence 23, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-23
Query Match      100.0%; Score 2180; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQRAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQRAGSGSRDDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPEPRPVDIGSGGFDVGALSLRGADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
Db 121 LRPEPRPVDIGSGGFDVGALSLRGADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGGPKPLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGGPKPLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 4

US-09-561-756-30
; Sequence 30, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; PRIOR FILING DATE: 2000-04-26
; PRIOR FILING DATE: 09/227,721
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQRAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQRAGSGSRDDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPEPRPVDIGSGGFDVGALSLRGADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
Db 121 LRPEPRPVDIGSGGFDVGALSLRGADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGGPKPLFFIQACGGEQKDHGFEVAS 300

Db 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGGPKPLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 5

US-09-227-721-30
; Sequence 30, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQRAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQRAGSGSRDDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPEPRPVDIGSGGFDVGALSLRGADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
Db 121 LRPEPRPVDIGSGGFDVGALSLRGADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGGPKPLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGGPKPLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 6

US-09-954-697-30
; Sequence 30, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697

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; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30

Query Match      98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDALLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFTISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
DB 61 DLETRGSQALPLFTISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESIRGNADLAYILSMPCGHCLIIINNPNFCRESGLRTR 180
DB 121 LRPETPRPVDIGSGGFGDVGALESIRGNADLAYILSMPCGHCLIIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSHFVVEVKGDLTAKXWVLLALLELARDHGDALDCCVVVILSHGQQ 240
DB 181 TGSNIDCEKLRRLRRFSSHFVVEVKGDLTAKXWVLLALLELARDHGDALDCCVVVILSHGQQ 240
QY 241 ASHLOFGAVGTDCGCVSVKEIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
DB 241 ASHLOFGAVGTDCGCVSVKEIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPEDSPGNSPEPDATPFQEGRLTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
DB 301 TSPEDSPGNSPEPDATPFQEGRLTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 7
US-09-257-218-2
; Sequence 2, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-257-218-2

Query Match      98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDALLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFTISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
DB 61 DLETRGSQALPLFTISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESIRGNADLAYILSMPCGHCLIIINNPNFCRESGLRTR 180
DB 121 LRPETPRPVDIGSGGFGDVGALESIRGNADLAYILSMPCGHCLIIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSHFVVEVKGDLTAKXWVLLALLELARDHGDALDCCVVVILSHGQQ 240
DB 181 TGSNIDCEKLRRLRRFSSHFVVEVKGDLTAKXWVLLALLELARDHGDALDCCVVVILSHGQQ 240
QY 241 ASHLOFGAVGTDCGCVSVKEIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
DB 241 ASHLOFGAVGTDCGCVSVKEIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPEDSPGNSPEPDATPFQEGRLTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
DB 301 TSPEDSPGNSPEPDATPFQEGRLTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 8
US-09-311-760-2
; Sequence 2, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
; FILING DATE: 13-May-1999
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-311-760-2

Query Match          98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVEELQVDOLMDVLLSRELFRPHMIEDIORAGSGSRDQARQLII 60
DB 1 MDEADRLRLRRCLRLVEELQVDOLMDVLLSSELFRPHMIEDIORAGSGSRDQARQLII 60
QY 61 DLETGSGQALPLFTSCLEDTGQDMLASFLRNRQAGKLSKPTLENLTPVVLRLPPIRKEPV 120
DB 61 DLETGSGQALPLFTSCLEDTGQDMLASFLRNRQAGKLSKPTLENLTPVVLRLPPIRKEPV 120
QY 121 LRPEPRPVDIGSGGFDGVALESIRGNADLAYILSMPECHGCLIIINNVPFCRESGLRTR 180
DB 121 LRPEPRPVDIGSGGFDGVALESIRGNADLAYILSMPECHGCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCG 240
DB 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCG 240
QY 241 ASHLQFPAGVYGTGDCPVSVKEIWNIFNGTSCPSLGGKPKLFFIQAACGGQKDHGFVEAS 300
DB 241 ASHLQFPAGVYGTGDCPVSVKEIWNIFNGTSCPSLGGKPKLFFIQAACGGQKDHGFVEAS 300
QY 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFFPGFVSWRDPKSG 360
DB 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 9
US-08-865-579-2
; Sequence 2, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-865-579-2

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Query Match          98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVEELQVDOLMDVLLSRELFRPHMIEDIORAGSGSRDQARQLII 60
DB 1 MDEADRLRLRRCLRLVEELQVDOLMDVLLSSELFRPHMIEDIORAGSGSRDQARQLII 60
QY 61 DLETGSGQALPLFTSCLEDTGQDMLASFLRNRQAGKLSKPTLENLTPVVLRLPPIRKEPV 120
DB 61 DLETGSGQALPLFTSCLEDTGQDMLASFLRNRQAGKLSKPTLENLTPVVLRLPPIRKEPV 120
QY 121 LRPEPRPVDIGSGGFDGVALESIRGNADLAYILSMPECHGCLIIINNVPFCRESGLRTR 180
DB 121 LRPEPRPVDIGSGGFDGVALESIRGNADLAYILSMPECHGCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCG 240
DB 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCG 240
QY 241 ASHLQFPAGVYGTGDCPVSVKEIWNIFNGTSCPSLGGKPKLFFIQAACGGQKDHGFVEAS 300
DB 241 ASHLQFPAGVYGTGDCPVSVKEIWNIFNGTSCPSLGGKPKLFFIQAACGGQKDHGFVEAS 300
QY 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFFPGFVSWRDPKSG 360
DB 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

```

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RESULT 10
US-10-059-749-2
; Sequence 2, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

```



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; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,308
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: 19840 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-7262
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-964-308-6

Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3.6e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHCLIIINNVCRESGLRTRTGSNIDCEKLRFRSSLHFMVVEVKGDLTA 209
Db 34 DNSYKMDYPMGLCIIINNKNFHKTGTSRGTDVDAANLRETFRNLYKYEVRNKNDLTR 93
QY 210 KMWLALLELARQDHGALDCCVVILSHGCOASHLQFPFVAVYGTDCGCVSVKEKIVNIFNG 269
Db 94 BEIVELMRDVSKEDHSKRSSFVCLLSHGEE-----GIIFGTNG-PVDLKKIINFRRG 145
QY 270 TSCPSLGGKPKLFFIQACGGEGKHGFVASTSPEDSPGSGNPEPDATPFQEGLETFDQL 329
Db 146 DCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182
QY 330 DAISLPTPSDFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEOWAHSEDLQSLLRVAN 389
Db 183 -ACHKIPVEADFLYASTAPGYYSWRNSKDGSGWFIQSLCAMLKQYADKLEFPHILTRVNR 241
QY 390 AVSVK-----GIYKQMPGCFNFKLFF 413
Db 242 KVATEFESFSDATFHAKKQIPCIIVSMLTKELYF 275

Search completed: August 3, 2004, 08:55:37
Job time : 20 secs
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RESULT 15
US-08-462-969B-4
; Sequence 4, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:59:31 ; Search time 16 Seconds
(without alignments)
2500.980 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKQPGCFNFKLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 208102

Minimum DB seq length: 0

Maximum DB seq length: 416

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	2	G02635
2	429	19.7	277	2	S64710
3	418	19.2	277	2	A55315
4	408	18.7	277	2	J05410
5	384	17.6	212	2	I67437
6	304	13.9	312	2	B54821
7	268.5	12.3	402	2	A46495
8	262	12.0	182	2	I67436
9	259	11.9	404	2	A42677
10	256.5	11.8	383	2	A56084
11	239.5	11.0	242	2	J07517
12	220	10.1	311	2	B56084
13	209	9.6	377	2	A57511
14	186	8.5	263	2	C56084
15	154.5	7.1	149	2	T43637
16	151.5	6.9	136	2	I53300
17	115.5	5.3	394	2	T26968
18	107.5	4.9	139	2	T43642
19	96.5	4.4	369	2	T32781
20	91.5	4.2	376	2	J07759
21	89.5	4.1	395	2	T05906
22	89	4.1	369	2	T20505
23	85.5	3.9	273	2	D84195
24	84.5	3.9	311	2	D75405
25	84.5	3.9	317	2	A59292
26	84	3.9	276	2	A0485
27	83	3.8	351	2	T25448
28	83	3.8	364	2	F83278
29	81.5	3.7	210	2	AG0534

30 81 3.7 163 1 JQ0144
31 81 3.7 163 2 F82988
32 80.5 3.7 345 2 JQ0429
33 80.5 3.7 361 2 T38693
34 80 3.7 288 2 A87051
35 80 3.7 375 2 S28739
36 79.5 3.6 195 2 S28739
37 79.5 3.6 284 2 G87701
38 79.5 3.6 375 1 S62638
39 79.5 3.6 381 2 G96804
40 79 3.6 191 2 T09985
41 79 3.6 398 2 H81090
42 78.5 3.6 328 2 S53336
43 78.5 3.6 350 1 ADECHF
44 78.5 3.6 350 2 F90726
45 78.5 3.6 350 2 G85577

ALIGNMENTS

RESULT 1

G02635

ICE-LAP6 - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C:Accession: G02635

R:Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit, V.

submitted to the EMBL Data Library, April 1996

A:Reference number: H01513

A:Accession: G02635

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-416 <DUA>

A:Cross-references: EMBL:U56390; NID:gl336026; PIDN:AAC50640.1; PID:gl336027

Query Match 100.0%; Score 2180; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 8 6e-179;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETRGSOALPLFTSCLEDTGQDMLASFLRTNQAGLSKPTLENLTPVVLREIRKPEV 120
Db 61 DLETRGSOALPLFTSCLEDTGQDMLASFLRTNQAGLSKPTLENLTPVVLREIRKPEV 120
Qy 121 LRPEPRPVDIGSGGFGDVGALSLRGNADLAVILSMPCGHCLIIINNVCRESGURTR 180
Db 121 LRPEPRPVDIGSGGFGDVGALSLRGNADLAVILSMPCGHCLIIINNVCRESGURTR 180
Qy 181 TGSNIDCEKLRRPFSLSHFVVEKGLDTAKKQVLALELARQDHGALDCCVWLSHGQC 240
Db 181 TGSNIDCEKLRRPFSLSHFVVEKGLDTAKKQVLALELARQDHGALDCCVWLSHGQC 240
Qy 241 ASHLQPGAVYGTGCPVSEKIVNFNGTSCPSLGKPKLFTFIQACGGKQDHGFVEAS 300
Db 241 ASHLQPGAVYGTGCPVSEKIVNFNGTSCPSLGKPKLFTFIQACGGKQDHGFVEAS 300
Qy 301 TSPEDSPGSNPEPDATPQEGRLTFDQLDAISSLTPSDIFVSYSTFPFGVSWRDPKSG 360
Db 301 TSPEDSPGSNPEPDATPQEGRLTFDQLDAISSLTPSDIFVSYSTFPFGVSWRDPKSG 360
Qy 361 SWYVETLDDIFQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 2

S64710

cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster

C:Species: Cricetulus griseus (Chinese hamster)

C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C/Accession: S64710; S72395
R/Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A/Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
A/Reference number: S64710; MUID:96183185; PMID:8605870
A/Accession: S64710
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-277 <WAN>
A/Cross-references: EMBL:U27463
R/Wang, X.
submitted to the EMBL Data Library, May 1995
A/Reference number: S72395
A/Accession: S72395
A/Molecule type: mRNA
A/Residues: 1-79, 'A', 81-146, 'Y', 148-277 <WAW>
A/Cross-references: EMBL:U27463; NID:g1244443; PIDN:AAB01511.1; PID:g1244444
C/Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match	19.7%	Score 429;	DB 2;	Length 277;	
Best Local Similarity	33.2%	Pred. No. 5.1e-29;			
Matches 91; Conservative 51;	Mismatches 90;	Indels 42;	Gaps 4		
Qy	150	DLAYILSWEPGCGHLLIINNWFRCRESGLURITGSNIDCEKLRFRPSSLHFVWVKGDLTA	209		
Db	34	DSSYKMDYPENGVCIIINNKFHKSTGMTPRSGTDVDAAKLRETFNNLKYEVRNKNIDLR	93		
Qy	210	KKMVLALLELARODHGALDCCVWILSHGCAASHLQFPQVYGTGDCPVSEKIVNIENG	269		
Db	94	EEIVELMKNAKEDHSEKRSFVCVILSHGDE-----GVIFGTDG-FIDLKLTSTPYFG	145		
Qy	270	TSCPSLGGKPKLFTIQAACGGQKHGFVASTSPEDSPGNSPEPDATPFQGLRTTFQOL	329		
Db	146	DRCSRLIGKPKLFIQAACRGTELDGCIETDSGTEDDMT-----	183		
Qy	330	DAISLTPPSDIFVSYSTFPFGVSRWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVAN	389		
Db	184	--CQKIPVEADFLVAYSTAPGYYSWRNPKDGSWFIQSLCSMLKLYAHKLEFPHILTVNR	241		
Qy	390	AVSVK-----GIYKQMPGCGCFNLRKKLFF	413		
Db	242	KVATFEFSFLSDSTPHAKKQIPICVISMLTKELFY	275		

RESULT 3

A53315
cysteine proteinase [EC 3.4.22.-] CPP32 precursor - human
N/Alternate names: cysteine proteinase CPP32
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence revision 06-Feb-1995 #text_change 01-Dec-2000
C/Accession: A53315; S58899; I39005
R/Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A/Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
A/Reference number: A53315; MUID:95074098; PMID:7983002
A/Accession: A53315
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-277 <PEP>
A/Cross-references: GB:U13737; MID:g561665; PIDN:AAAG5015.1; PID:g561666
R/Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.;
Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A/Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalia
A/Reference number: S58899; MUID:95319529; PMID:7596430
A/Accession: S58899
A/Molecule type: protein
A/Residues: 29-46/176-189, 'E', 191-193 <NIC>
R/Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier
Cell 81, 801-809, 1995
A/Title: Yama/ CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
A/Reference number: A56924; MUID:95292347; PMID:7774019

[illegible]

RESULT 4

JC5410

CPp32 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

C:Accession: JC5410

R:Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.

Biochem. Biophys. Res. Commun. 231, 770-774, 1997

A:Title: Specific expression of CPp32 in sensory neurons of mouse embryos and

A:Reference number: JC5410; MUID:97224429; PMID:9070890

A:Accession: JC5410

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-277 <MOK>

A:Cross-references: DDBJ:D86352

A:Experimental source: embryo

C:Comment: This protein is involved in the apoptosis of dorsal root ganglia ne

Query Match	18.7%	Score 408;	DB 2;	Length 277;	
Best Local Similarity	32.1%	Pred. No. 3.2e-27;			
Matches	88;	Conservative 52;	Mismatches 9;	Indels 42;	Gaps 4
QY	150	DLAVILSMPECHCHLIIINNFCRESGLRTRGTGNSIDCEKILRRRPFSSLIHFVVEVKGDLTA	209		
DB	34	DSSYKMDYPENGICIIITKNFKHSTGWSRSRGTDVDAANRETPEMGLKYEVRNKNDLTR	93		
QY	210	KKWVLALELARQDHGALDCVVILSHGCOASHLQFPGAVYGTGCPVSEKIVNIENG	269		
DB	94	EEIMELMDSVSKEDHSKSSFCVLLSHGDE-----GVIFGNG-PVDLKKLTSFPG	145		
QY	270	TSCPSLGGKPKLFFIIQACGGQKHGFVASTPEDESGPNSPEPDATFPOEGLTFDQL	329		
DB	146	DYCRSLTGKPKLFIQACRGTELDCCIETSDGTDEEM-----	182		
QY	330	DAISSLPESDIFVSYSITFGPVSWRDKSGSWYVETLDDIFEOAWHSEDLSLLLRVAN	389		
DB	183	-ACQKIPVEADFLYAYSTAPGGYSWRNSKDSWFIQSLCSMLKLYAHKLEFMHILTVNR	241		
QY	390	AVSVK-----GIYKOMPQCFNIRKKLFF	413		
DB	242	KVATFEGFSLDSTPHAKKQICIVSMILTKELYF	275		


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QY 213 VLALLELAR-QDHGALDCCVVVILSHGCOASHLQFPGAVYTGDCPV-SVEKIVNIENG 270
Db 211 VKEVKEFAACPEHKTSOSTFLVFMSHGIQEG---ICGTTYGNEVSDILKVDTFIQMMNTL 267
QY 271 SCPSLGKPKLFFFTQACCGEOKDHCFEAVASTSPDESFGSNPEPDATPFQGLRT---FD 327
Db 268 KCPSLKOKPKVILIIQACGKQ--GVVLLKDSVRDS-----EDFLTDALFE 312
QY 328 QLDAISSLPTSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRV 387
Db 313 D-DGKKAHIEKDFIAFCSTPDNVSWRHPVRSGLFIESLHKMKEYAWSODLEDIFRKV 371
QY 388 ANAVSVKGIYKQPCFNLKRLFF 413
Db 372 RFSFQEPFRLQMPADRVTLLTKREY 397

RESULT 8
I67436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I67436
R:Flaws, J.A.; Kugy, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Til
Endocrinology 136, 5042-5053, 1995
A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nuloa cells of the ovarian follicle.
A:Reference number: I53300; MUID:96042508; PMID:7588240
A:Accession: I67436
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-182 <RES>
A:Cross-references: EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g1004369

Query Match 12.0%; Score 262; DB 2; Length 182;
Best Local Similarity 33.3%; Pred. No. 5.9e-15;
Matches 63; Conservative 33; Mismatches 75; Indels 18; Gaps 4;
QY 159 PGGHCLIIINNFCRESGLRTTGSNIDCEKLRFPSSLHFVVEVKGDITAKKVVALLLE 218
Db 1 PRGLALVMSNVHFTGKDLFRSGVDVHTTLVTLFLKLLGVNVHVLVDQTAQEMOKLQ 60
QY 219 LAR-QDHGALDCCVVVILSHGCOASHLQFPGAVYTGDCPVSEKIVNIFNGTSCPSLGG 277
Db 61 FAQLPAHRVTDSCIVALLSHGVE-----GGYIGVDGKLLQCEVRLFDNANCPSLQ 113
QY 278 KPKLFFIQCGGQKDHGFEVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPT 337
Db 114 KPMFFIQACRGDETDRGVDDQDGKHAQPPGC--EESDTVKEELMK-----MRLPT 163
QY 338 PSDIFVSYS 346
Db 164 RSDMICVYA 172

RESULT 9
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: A54263; A42677; S21734; S24164
R:Gerrett, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
Genomics 20, 468-473, 1994
A:Title: Molecular characterization of the gene for human interleukin-1beta converting e
A:Reference number: A54263; MUID:94307734; PMID:8034320
A:Accession: A54263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-404 <CE2>
A:Cross-references: GB:L27475
R:Gerrett, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992
A:Title: Molecular cloning of the interleukin-1beta converting enzyme.
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A:Reference number: A42677; MUID:92229430; PMID:1373520
A:Accession: A42677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <CER>
A:Cross-references: GB:M87507; NID:g435598; PIDN:AAA66942.1; PID:g186286
R:Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.;
J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Lamjuco, G.; Palyha, O.C.; Raju, S.M.; Rol
cci, M.J.
Nature 356, 768-774, 1992
A:Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proce
A:Reference number: S21734; MUID:92244338; PMID:1574116
A:Accession: S21734
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <THO>
A:Cross-references: EMBL:X65019; NID:g33792; PIDN:CAA46153.1; PID:g33793
R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992
A:Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
A:Reference number: S24164; MUID:92337439; PMID:1321594
A:Accession: S24164
A:Status: preliminary
A:Molecule type: protein
A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
C:Genetics:
A:Gene: GDB:ILLABC
A:Cross-references: GDB:132368; OMIM:147678
A:Map position: 11q23-11q23
C:Keywords: cysteine proteinase; hydrolase

Query Match 11.9%; Score 259; DB 2; Length 404;
Best Local Similarity 24.3%; Pred. No. 3.1e-14;
Matches 104; Conservative 62; Mismatches 176; Indels 86; Gaps 14;
QY 10 RCRRLRVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRDQARQLIIDLETRGSA 69
Db 10 RKLFRSNGEGTINGLLDELQTRVLNKEEMKVKRE-NATVMDKTRALIDSVIPKGAQA 68
QY 70 LPLFIS--CLEP-----TGQDMLASFRTNRQAGLSKPTLENLTFVVLRLPEIRKP 118
Db 69 CQICITYICEEDSYLAGTLGJSADOTSGNYLNNQSQGVLS-----SFPAP 114
QY 119 EYLRPETPRPVDIGSGGFDVGALRESL-----RGNADLAYILSMPCGH-CLIIINNVPFC 172
Db 115 QAVQNPAPTSSSGEGNVKLSLEAQRIWKQSAEIVPIMDKSRTRLALICNEEF- 173
QY 173 RESGLRTRTGSNIDCEKLRFRFSSLHFVVEVKGDITAKKVVALLLELA-RQDHGALDCCV 231
Db 174 --DSIPRRTGAEDVITGMTLLQLNGYSVDVKKNLTASDMTTELEFAHRPEKTSdstf 231
QY 232 VVILSHG-----CQASHL-QFFGAVYTGDCPVSEKIVNIFNGTSCPSLGGKPKLFFIQ 285
Db 232 LVFMHSHGIREG:CGKKHSEQVPDI-----LQNLAI FNM LNTKNCPSLKKPKVILIQ 283
QY 286 ACGEQKDHGFEVASTSPDESFP-----GSNPEPDATPFQGLRTFDQLDAIS 333
Db 284 ACRG-----DSFGVVWFKDSVGSVGNLSLPTTEEFED-----DAIK 319
QY 334 SLPTPSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSV 393
Db 320 KAHIEKDFIAFCSTPDNVSWRHPRTMGVSFVIGRLIEHMQEYACSCDVERIFRKVRFSFEQ 379
QY 394 KGIYKOMP 401
Db 380 PDGRAOMP 387

RESULT 10
A56084
interleukin-1beta converting enzyme beta isozyme - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
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C;Species: Homo sapiens (man)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 08-Oct-1999
A;Accession: A57511; S55257
R;Munday, N.A.; Vaillancourt, J.P.; Ali, A.; Casano, F.J.; Miller, D.K.; Molineaux, S.M.
J. Biol. Chem. 270, 15870-15876, 1995
A;Title: Molecular cloning and pro-apoptotic activity of ICE-relII and ICE-relIII, members of the ICE-rel family
A;Reference number: A57511; MUID:95318183; PMID:7797592
A;Accession: A57511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-377 <MUN>
A;Cross-references: GB:U28014; NID:g975299; PIDN:AAA75171.1; PID:g903934
R;Faucheu, C.; Dia, A.; Chan, A.W.E.; Blanchet, A.M.; Miossec, C.; Herve, F.; Collard-Duval, J.D.
EMBO J. 14, 1914-1922, 1995
A;Title: A novel human protease similar to the interleukin-1-beta converting enzyme inducible
A;Reference number: S55257; MUID:95262631; PMID:7743998
A;Accession: S55257
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-377 <FAU>
A;Cross-references: GB:Z48810; GB:S78281; NID:g999453; PIDN:CAA88750.1; PID:g999454
C;Keywords: cysteine proteinase; hydrolase

Query Match 9.6%; Score 209; DB 2; Length 377;
Best Local Similarity 21.9%; Pred. No. 5.5e-10;
Matches 95; Conservative 63; Mismatches 154; Indels 122; Gaps 14;

QY 10 RRCRLRVEELQVQLMDVLLSRELFRPHMIEDIQRAGSGRRDQARQLIIDLETRGSQA 69
DB 7 RKKPLKVLSELGKQFLTGVL-----DNLVEQVNLWKEEKKYYDAKT----- 50
QY 70 LPLFISCLEDTGQDMLASFLRTNQAGKLSKPTLENLTPVLRPEIR-KPEVLRPETPRP 128
DB 51 -----EDKVRVMADSMQEKQRMAGQMLLTQTFNIDQISPNKKAHPMNEAGPPGES 102
QY 129 VDIGSGGPDVGALSLRGADLAVILSMPCGH----- 162
DB 103 TD-----ALKLPHEEFRLCKERAEEIYPIKERNRRL 137
QY 163 CLIIINNVCRESGLRRTGSDNICELRRRFSLLHFMVYKGDITAKKVMVLALLELA-R 221
DB 138 ALIICNTEF---DHLPPRGADFDITGMKELLEGDYSVDVEENLTARDMESALRAFATR 194
QY 222 QDHGALDCCVVILSHG-----CQASHLPFGAVYGTGCPVSVEKIIVNFGTSCPSLG 276
DB 195 PEKSSDSTFLVMSHGILGICGTVDHDEKRPD-----LLYDTIFQIFNNRNCLSLK 247
QY 277 GKPKLFFIQACGGEQKH-----GFEVASTSPEDSPGSNPPDPATPFQEGRLTFDQ 328
DB 248 DKPKVLIQACRGANRGELWVRDSPALESVASSQSSE-----NLEEDAV-----YKTHVE 297
QY 329 LDAISSLPTPSDIFVSY-STFPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRV 387
DB 298 KD-----FIAPCSSTPHNVSRDSTMGSTFIQTLCFCQKYSWCCHLEVRKV 346
QY 388 ANAVSVKGIYKOMP 401
DB 347 QQSFPETPRAKQMP 360

RESULT 14
C56084
Interleukin-1beta converting enzyme delta isozyme - human
C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
A;Accession: C56084
R;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A;Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver
A;Reference number: A56084; MUID:95181414; PMID:7876192
A;Accession: C56084
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-263 <ALN>
A;Cross-references: GB:U13699; NID:g717043; PIDN:AAC50109.1; PID:g717044
C;Genetics:
A;Gene: IL1BCE
C;Keywords: alternative splicing

Query Match 8.5%; Score 186; DB 2; Length 263;
Best Local Similarity 22.4%; Pred. No. 3.1e-08;
Matches 71; Conservative 43; Mismatches 119; Indels 84; Gaps 8;

QY 98 LSKPTLENLPVLRPEIRKPEVLRPETPRVDIGSGGFGDVGALSL-----RGNADLA 152
DB 1 MADKVLKEKKLFRSNGEAPQAVODNPAMPTSSGSEGNVKLCSLEAQRWVKQSAIY 60
QY 153 YILSMPCGH-CLIIINNVCRESGLRRTGSDNICELRRRFSLLHFMVYKGDITAKK 211
DB 61 PIMDKSSRTRLLALICNEEF---DSIPRRTGAEDITGMTLLQLNLGYSDVVKKNTASD 117
QY 212 MYLALLELA-RQDHGALDCCVVILSHG-----CQASHL-QFPGNAVYGTGCPVSVEKIV 264
DB 118 MTTELEAFARPEKHTSDSTFLVMSHGIREGICGKHSEGVPI-----LQNLNIF 169
QY 265 NIFNGTSCPSLGGKPKLFFIQACGGEQKHDEGFEVASTSPEDSPGSNPPDPATPFQGLR 324
DB 170 NMLTKNCPSLKDKPKVILIIQACRGDN----- 196
QY 325 TFDQLDAISSLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLL 384
DB 197 -----VSWRHPTMGSVFIIIGRLIEHMQEYACSCDVEEIF 229
QY 385 LRVANAVSVKGIYKOMP 401
DB 230 RKVRFSEPDGDAQMP 246

RESULT 15
T43637
Caspase protein 1C - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
A;Accession: T43637
R;Shaham, S.
J. Biol. Chem. 273, 35109-35117, 1998
A;Title: Identification of multiple Caenorhabditis elegans caspases and their potential
A;Reference number: Z22587; MUID:99074291; PMID:9857046
A;Accession: T43637
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-149 <SHA>
A;Cross-references: EMBL:AF088287; NID:g4063371; PIDN:AAC98294.1; PID:g4063372
C;Genetics:
A;Note: csp-1

Query Match 7.1%; Score 154.5; DB 2; Length 149;
Best Local Similarity 31.5%; Pred. No. 7.2e-06;
Matches 45; Conservative 24; Mismatches 61; Indels 13; Gaps 4;

QY 153 YILSMPCGHCLIIINNVCRESGLRRTGSDNICELRRRFSLLHFMVYKGDITAKK 212
DB 17 YEMNSNFRGTVLIIISNENF---KNMRRVGTQKQDEVNLTKLQKLYQYTVICKRNLEASM 73
QY 213 VLALLELARQDHGALDCCVVILSHGCOASHLPFGAVYGTGCPVSVEKIVNFGTSC 272
DB 74 LEAKKEFAEMAH--TDSILFLSHGDA-----GSVFGIDDMFVNVMVEYSTYL--AYH 123
QY 273 PSLGGKPKLFFIQACGGEQKHG 295
DB 124 QNLLLPKPKWAVSACRGKIEHG 146

Search completed: August 3, 2004, 09:03:10
Job time : 18 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2004, 08:55:41 ; Search time 13 Seconds
(without alignments)
1666.245 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 2180
Sequence: 1 MDEADRLRLRCRLRLBEL.....YKQMPGCFNLRKKLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 98277

Minimum DB seq length: 0
Maximum DB seq length: 416

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2166	99.4	416	1 ICE9 HUMAN	P55211 homo sapien
2	428	19.6	277	1 ICE3_XENLA	Q60431 cricetulus
3	418	19.2	277	1 ICE3_HUMAN	P42574 homo sapien
4	409	19.2	277	1 ICE3_MOUSE	P70677 mus musculus
5	364.5	16.7	303	1 ICE3 RAT	P55213 rattus norv
6	364.5	16.7	303	1 ICE7_MESAU	P55214 mesocricetu
7	361.5	16.6	303	1 ICE7_HUMAN	P55210 homo sapien
8	350.5	16.1	303	1 ICE7_MOUSE	P97864 mus musculus
9	349	16.0	282	1 ICE3_XENLA	P55866 xenopus lae
10	324	14.9	339	1 ICE_MOUSE	O01382 drosophila
11	322	14.8	276	1 ICE6_MOUSE	O08738 mus musculus
12	320	14.7	323	1 ICE1_DROME	O02002 drosophila
13	312.5	14.3	312	1 ICE2 RAT	P55215 rattus norv
14	311.5	14.3	293	1 ICE6_HUMAN	P55212 homo sapien
15	300.5	13.8	405	1 ILBC_HORSE	Q9tw13 equus caball
16	297.5	13.6	299	1 ICE1_SPOFR	P89116 spodoptera
17	279	12.8	382	1 ICEB_XENLA	P55867 xenopus lae
18	278	12.8	404	1 ILBC_PIG	Q9n311 sus scrofa
19	274	12.6	410	1 ILBC_FELCA	Q9mzv6 felis silve
20	270.5	12.4	402	1 ILBC RAT	P43527 rattus norv
21	268.5	12.3	402	1 ILBC_MOUSE	P29452 mus musculus
22	262	12.0	404	1 ILBC_CANFA	Q9mzv7 canis fami
23	259	11.9	404	1 ILBC_HUMAN	P29466 homo sapien
24	256	11.7	386	1 ICEA_XENLA	P55865 xenopus lae
25	253	11.6	257	1 ICEE_MOUSE	O89094 mus musculus
26	239.5	11.0	242	1 ICEE_HUMAN	P31944 homo sapien
27	232	10.6	377	1 ICED_BOVIN	O75601 bos taurus
28	212	9.7	373	1 ICE4_MOUSE	P70343 mus musculus
29	209	9.6	377	1 ICE4_HUMAN	P49652 homo sapien
30	97.5	4.5	382	1 AMAC_HUMAN	Q9uhk6 homo sapien
31	83.5	3.8	199	1 CRAD_MOUSE	O88843 mus musculus
32	83.5	3.8	410	1 AUP1_MOUSE	P70295 mus musculus
33	81	3.7	163	1 DSB1_PSEAE	P21482 pseudomonas

34	81	3.7	371	1 PGLR_PENJA	O42824 penicillium
35	80.5	3.7	345	1 YT37_STRFR	P20187 streptomyce
36	80.5	3.7	375	1 ADHH_GADMO	P81600 gadus morhu
37	80	3.7	288	1 HBWK_MYCLE	P45832 mycobacteri
38	80	3.7	291	1 FPG_PROMM	Q7v8y5 prochloroco
39	79.5	3.6	375	1 ADHA_UROHA	P25405 uromastys h
40	79	3.6	398	1 ARGD_NEIMB	Q9jyy4 neisseria m
41	78.5	3.6	290	1 SYGA_FUSNN	Q8rh45 fusobacteri
42	78.5	3.6	328	1 CEBB_CHICK	P05826 gallus gall
43	78.5	3.6	350	1 AROG_ECOLI	P00886 escherichia
44	78.5	3.6	363	1 GCST_HALNI	Q9hpj7 halobacteri
45	78	3.6	199	1 CRAD_HUMAN	P78560 homo sapien

ALIGNMENTS

RESULT 1
ICE9 HUMAN
ID ICE9 HUMAN STANDARD; PRT; 416 AA.
AC P55211; Q95348; Q92852; Q9BQ62; Q9UEQ3; Q9UIJ8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic
protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease
activating factor 3) (APAF-3).
GN CASP9 OR MCH6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=96279246; PubMed=8663294;
RA Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,
RA He W.-W., Dixit V.M.;
RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated
by the cytotoxic T cell protease granzyme B.";
RL J. Biol. Chem. 271:16720-16724(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.
RC TISSUE=L-cell;
RX MEDLINE=97059171; PubMed=8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
mediator CPP32.";
RL J. Biol. Chem. 271:27099-27106(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315341; PubMed=10384055;
RA Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P.,
RA Sherer S.W., Beatty B.G., Ikeda J.B., Nicholson D.W., Hayden M.R.;
RT "Genomic organization of the human caspase-9 gene on chromosome
1p36.1-p36.3";
RL Mamm. Genome 10:757-760(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99168502; PubMed=10070954;
RA Srinivasula S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification of an endogenous dominant-negative short isoform of
caspase-9 that can regulate apoptosis.";
RL Cancer Res. 59:999-1002(1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX TISSUE=Stomach cancer;
RA Izawa M., Mori T., Ito H., Saitenji T.;
RT "Molecular cloning and sequencing of a cDNA predicting an alternative
form of pro-caspase-9 from human gastric cancer cell lines.";


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Query Match 99.4%; Score 2166; DB 1; Length 416;
Best Local Similarity 99.3%; Pred. No. 8.4e-177;
Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEARRLLRCRLRLVEELQVDLQDVLRLSRLFRPHMIEDIORAGSGSRDDQAROLII 60
DB 1 MDEARRLLRCRLRLVEELQVDLQDVLRLSRLFRPHMIEDIORAGSGSRDDQAROLII 60
QY 61 DLETRGSQALPLFISCLDGTGDMLASFLRNQRAKLSKPTLENLTPVILRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTGDMLASFLRNQRAKLSKPTLENLTPVILRPEIRKPEV 120
QY 121 LRPETPRPVDGSGFGDVGALSRGNADLAILSMPEPCGCHLIINNVPFCRESGLRTR 180
DB 121 LRPETPRPVDGSGFGDVGALSRGNADLAILSMPEPCGCHLIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRFRFSLHFMVEKGLTAKKMWLALLLRLARODHGALDCCVVILSHGCQ 240
DB 181 TGSNIDCEKLRFRFSLHFMVEKGLTAKKMWLALLLRLARODHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFVAS 300
DB 241 ASHLQFPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFVAS 300
QY 301 TSPDESPGSPNEPDATPFQGLRTFDQDLAISLTPSDIFVSYSTPFGFVSWRDPKSG 360
DB 301 TSPDESPGSPNEPDATPFQGLRTFDQDLAISLTPSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDQLSLLRVANAVSVKGYKQMPGCFNLRKKLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDQLSLLRVANAVSVKGYKQMPGCFNLRKKLFFKTS 416

RESULT 2
ICE3_CRILLO STANDARD; PRT; 277 AA.
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1) OR CPP32.
GN Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96183185; PubMed=8605870;
RA Wang X., Zelenski N.G., Yang J., Sakai J., Brown M.S.,
RA Goldstein J.L.;
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis.";
RL EMBO J. 15:1012-1020(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- FTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=t-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
RT interleukin-1 beta-converting enzyme.";
RL J. Biol. Chem. 269:30761-30764(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Foirier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Foirier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [4]
RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Foirier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [5]
RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Foirier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [6]
RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Foirier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=96266352; PubMed=8673606;
RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
RA Labelle M., Peterson B.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
RA Thornberry N.A., Becker J.W.;
RT "The three-dimensional structure of apopain/CPP32, a key mediator of
RT apoptosis.";
RN [8]
RN Nat. Struct. Biol. 3:619-625(1996).
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RP MEDLINE=97197830; PubMed=9045680;
RA Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
RA Priestle J.P., Tomaselli K.J., Gruetter M.G.;
RT "Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RL J. Biol. Chem. 272:6539-6547(1997).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberger Y.P., Nicholson D.W., Rasper D.M., Kallchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vaillancourt J.P., Hayden M.R.;
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449(1996).
RN [10]
RN FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates steryl regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9. Involved in the
CC cleavage of huntingtin.
CC -!- ENZYME REGULATION: Inhibited by isatin sulfonamides.
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC -!- PTM: CLEAVAGE BY GRANTZME B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL; U13737; AAA65015.1; -;
CC EMBL; U13738; AAA60355.1; -;
CC EMBL; U26943; AAA74929.1; -;
CC DR EMBL; U13737; AAA65015.1; -;
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DR EMBL: AY219866; A025654.1; -.
DR EMBL: BC016926; AAH16926.1; -.
DR PIR: A55315; A55315.
DR PDB: 1PAU; 07-JUL-97.
DR PDB: 1CP3; 24-DEC-97.
DR PDB: 1GFW; 23-JUN-00.
DR MEROPS: C14.003; -.
DR Genew; HGNC:1504; CASP3.
DR MIM; 600636; -.
DR GO: GO:0004208; F:caspase-3 activity; TAS.
DR GO: GO:0008624; P:induction of apoptosis by extracellular sig. . .; TAS.
DR GO: GO:0008629; P:induction of apoptosis by intracellular sig. . .; TAS.
DR GO: GO:0009405; P:pathogenesis; TAS.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR KX Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
KW 3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT VARIANT 190 190 D -> E (in isoform beta).
FT CONFLICT 31 36 ISLSDNS -> MSWDTG (IN REF. 3).
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT TURN 67 80
FT TURN 81 82

Query Match
Best Local Similarity 19.2%; Score 418; DB 1; Length 277;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMEPCGHCLIIINNFCRSGLRTRGTSNIDCEKLRFRFSSLHFVVEVKGDLTA 209
Db 34 DNSYKMDYPENGCLIIINNFKHSTGTSRSGTDVDAANLRETFNKLKYEVRNNDLTR 93
QY 210 KMWVALLLELARQDHGALDCCVWILSHGQASHLQFPFVAVYGTDCGCVSVKIVNIFNG 269
Db 94 EEIVELMRDVSXEDSHKSRSSFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFRFG 145
QY 270 TSCPSLGGKPKLFFFTQACGEGKXGFFVASTSPDESGPSNPEPDATPFQGLKTFDQL 329
Db 146 DRCRLSLTGKPKLFFITQACRGTELDGCIETDSGVDDM----- 182
QY 330 DAISLPLTPSDFVSYSTFPFGVSRVDPKSGSWYVETLDDIFEOAHSEDLSQALLRVAN 389
Db 183 -ACHKIPVDADFLAYSTAPGYISWRNSKDGWFIQSLCAMLKQVADKLEFHMHLITRVNR 241
QY 390 AVSVK-----GIYKMGPCFNFLRKLFF 413
Db 242 KVATEFESFSDATFHANKQIFCIVSMILTKEYLF 275

RESULT 4
ICE3 MOUSE
ID ICE3 MOUSE STANDARD; PRT; 277 AA.
AC P70677; 008668; Q9QW14;
DT 01-NOV-1997 (Rel. 35, Created)

```

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE).
GN CASP3 OR CPP32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070890;
RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF.";
RL Biochem. Biophys. Res. Commun. 231:770-774 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/An.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaabeele P., Declercq W., van den Brande I.,
RA van Ioo G., Molemans F., Schotte P., van Criekeinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69 (1997).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 58-277 FROM N.A.
RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
RA Fortin J.-P., Sekaly R.-P.;
RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it

```

CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.
 CC -1- PTM: CLEAVAGE BY GRANZYME B. CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC
 CC EMBL; U54803; AAC52768.1; -.
 CC EMBL; U54802; AAC52768.1; JOINED.
 CC EMBL; U49929; AAC52764.1; -.
 CC EMBL; D86352; BAAL1727.1; -.
 CC EMBL; Y13086; CAAY3528.1; -.
 CC EMBL; U19522; AAC53196.1; -.
 CC EMBL; BC038825; AAB38825.2; -.
 CC EMBL; U63720; AAD09504.1; -.
 CC PIR; JC5410; JC5410.
 CC HSSP; P42574; IPAU.
 CC MEROPS; C14.003; -.
 CC MGD; MGI:107739; Casp3.
 CC InterPro; IPR002138; ICE p10.
 CC InterPro; IPR001309; ICE p20.
 CC InterPro; IPR002398; Peptidase C14.
 CC Pfam; PF00656; Peptidase_C14; 1.
 CC PRINTS; PR00376; IULBENZIME.
 CC SMART; SM00115; CASc; 1.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS50207; CASPASE_P10; 1.
 CC PROSITE; PS50208; CASPASE_P20; 1.
 CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
 KW PROPEP 1 9 BY SIMILARITY.
 FT PROPEP 10 28 BY SIMILARITY.
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT CONFLICT 17 17 E -> G (IN REF. 2).
 FT CONFLICT 51 51 N -> T (IN REF. 2).
 FT CONFLICT 63 65 SRS -> ARN (IN REF. 6).
 FT CONFLICT 84 84 Q -> E (IN REF. 2).
 FT CONFLICT 95 95 D -> E (IN REF. 2).
 FT CONFLICT 97 97 L -> M (IN REF. 2).
 FT CONFLICT 128 128 Y -> F (IN REF. 2).
 FT CONFLICT 135 135 E -> D (IN REF. 2).
 FT CONFLICT 231 231 E -> Q (IN REF. 6).
 FT CONFLICT 262 262 I -> F (IN REF. 6).
 SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;
 Query Match 19.2%; Score 418; DB 1; Length 277;
 Best Local Similarity 32.8%; Pred. No. 3.5e-28;
 Matches 90; Conservative 50; Mismatches 92; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLIINNVNCRBSGLTRTGSNIDCEKLRERFSSLHFMVEVKGLTA 209
 Db 34 DSSYKMDYDEMGICIIINNNKFKSTGMSRSGTDVDAANLRETFMLGIYQVKNKDLTR 93
 QY 210 KKMVLALLBLARQDHGALDCCVVVILSHGCGQASHLQFGAVYGTDCGPVSVEKIVNIFNG 269
 Db 94 EBILELMDSVSKEDHSKRSFVCVILSHGDE-----GVYGTNG-PVELKLTSTFRG 145
 QY 270 TGCPISGGKPKLFFITQACGGEGKDHGFVASTSPEDSPGSPNPPDATPFQEGLRFTDQL 329
 Db 146 DYCRSLTGRPKLFIQACRGTELDGIEDTSDTEEM----- 182
 QY 330 DAISSLPTSDIFVSYSTPGFVSNEDPKSGWYVETLDDIPEQMAHSDQLQLLLRVAN 389
 Db 183 -ACQKIPVEDFLYAYSTAGYISWRNSKDGWFIOSLCSMLKLYAHKLEFHMILTRVN 241
 QY 390 AVSVK-----GIYKQMPGCFNLRKKLFF 413
 Db 242 KVATEFESFLDSTPHAKQIPCIIVSMLTKELVF 275
 RESULT 5
 ICE3_RAT STANDARD; PRT; 277 AA.
 AC P55213; P70543; P97699; O62993;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 GN CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3";
 RL Oncogene 13:749-755 (1996).
 RN [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
 RA Hirschfield A.N., Tilly J.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
 RT endonuclease activity from morphological apoptosis in granulosa cells
 RT of the ovarian follicle";
 RL Endocrinology 136:5042-5053 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184204; PubMed=9030616;
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
 RA Rostack P. Jr., Poirier G.G., Paul S.M.;
 RT "Cloning and expression of a rat brain interleukin-1-beta-converting
 RT enzyme (ICE)-related protease (IRP) and its possible role in
 RT apoptosis of cultured cerebellar granule neurons.";
 RL J. Neurosci. 17:1561-1569 (1997).
 RN [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it

CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
CC BUT NOT IN KIDNEY OR TESTIS.
CC -!- DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions
CC of the developing brain, but down-regulated to low levels in the
CC adult brain.
CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: U49930; AAC52765.1; -;
CC EMBL: U34685; AAC52261.1; -;
CC EMBL: U84410; AAB41792.1; -;
CC EMBL: U58656; AAB02722.1; -;
CC PIR: I67437; I67437.
CC HSP: P42574; 1PAU.
CC MEROPS: C14.003; -;
CC InterPro: IPR002138; ICE p10.
CC InterPro: IPR001309; ICE p20.
CC InterPro: IPR002398; Peptidase C14.
CC Pfam: PF00656; Peptidase C14; 1.
CC PRINTS: PR00376; ILIBCEZYME.
CC SMART: SM00115; CASC.1.
CC PROSITE: PS01122; CASPASE_CYS; 1.
CC PROSITE: PS01121; CASPASE_HIS; 1.
CC PROSITE: PS0207; CASPASE_P10; 1.
CC PROSITE: PS0208; CASPASE_P20; 1.
CC KW Hydrolyase; Thiol protease; Apoptosis.
CC FT PROPEP 1 9 BY SIMILARITY.
CC FT PROPEP 10 28 BY SIMILARITY.
CC FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
CC FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
CC FT ACT_SITE 121 121 BY SIMILARITY.
CC FT ACT_SITE 163 163 BY SIMILARITY.
CC FT CONFLICT 25 29 KSMDS -> QVD (IN REF. 4).
CC FT CONFLICT 170 170 C -> S (IN REF. 2).
CC FT CONFLICT 178 178 T -> A (IN REF. 2).
CC FT CONFLICT 182 182 M -> V (IN REF. 2).
CC FT CONFLICT 187 187 I -> K (IN REF. 2).
CC FT CONFLICT 190 190 E -> G (IN REF. 3).
CC FT CONFLICT 199 199 T -> S (IN REF. 2).
CC FT CONFLICT 211 211 D -> G (IN REF. 2).
CC FT CONFLICT 236 236 L -> I (IN REF. 4).
CC FT CONFLICT 245 245 T -> M (IN REF. 3).
CC SQ SEQUENCE 277 AA; 31491 MW; ADABF418E2507402 CRC64;

Query Match 18.8%; Score 409; DB 1; Length 277;
Best Local Similarity 32.1%; Pred. No. 2e-27;
Matches 88; Conservative 52; Mismatches 92; Indels 42; Gaps 4;
QY 150 DLAYILSMPECHGCLIIINNVNFCRESGLRTRGNSNIDCEKLRFRSSLHFMVEYKGLTA 209
DB 34 DSSYKMDYEMGLCIIIIINNNKFNHFKSTGMSARNGTDVDAANLRFTWALKYEVNKNDLTR 93

QY 210 KKMVLALLELARQDHGALDCCVVILSHGCOASHLQFFGAVYGTDCPVSVKEKIVNIFNG 269
DB 94 EIMELMDSVSKEDHSKRSSFVCLSHGDE-----GVIFGTNG-PVDLKLKLTSPFRG 145
QY 270 TSCPSLGGKPKLFFITQACGGFKQKHGPRVASTSPEDSPGSPNPEDATPFQEGRLTFQOL 329
DB 146 DYCRSLTKPKLFIQACRGTELDGCIETDGTDDM----- 182
QY 330 DAISLTPSPDIFVSYSYTFPGFVSWRDPKSGSWVETLDDIFEQWAHSEDLQSLLRVAN 389
DB 183 -ACQKIPVEADFLYAYSTAPGYSWRNSRDGSWFIQSLCAMLKLYAHKLEFMHILTVNR 241
QY 390 AVSVK-----GIYKMPGCFNFKLFF 413
DB 242 KVATEFESFSLDATPHAKKQIPCVISMLTKELYF 275
RESULT 6
ICE7_MESAU
ID ICE7_MESAU STANDARD; PRT; 303 AA.
AC P55214;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
DE (SCA-2).
GN CASP7 OR MCH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Syrian; TISSUE=Liver;
RX MEDLINE=96224303; PubMed=8643593;
RA Pai J.-T., Brown M.S., Goldstein J.L.;
RT "Purification and cDNA cloning of a second apoptosis-related cysteine
RT protease that cleaves and activates sterol regulatory element binding
RT proteins".
RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC regulatory element binding proteins (SREBPs). Proteolytically
CC cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-1-Gly-217
CC bond. Overexpression promotes programmed cell death (By
CC similarity).
CC -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC -----
CC EMBL: U47332; AAC52595.1; -;
CC DR HSSP; P42574; 1PAU.
CC DR MEROPS; C14.004; -;
CC DR InterPro: IPR002138; ICE p10.
CC DR InterPro: IPR001309; ICE p20.
CC DR InterPro: IPR002398; Peptidase C14.
CC DR Pfam; PF00656; Peptidase C14; 1.


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CC CPP32. PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32. PROTEASE ALSO OCCUR AND
CC VICE VERSA.
CC
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC
CC EMBL; U39613; AAC50346.1; -
CC EMBL; U40281; AAC50352.1; -
CC EMBL; U37448; AAC50303.1; -
CC EMBL; U37449; AAC50304.1; -
CC EMBL; U67319; AAC51152.1; -
CC EMBL; U67320; AAC51153.1; -
CC EMBL; U67206; AAF21460.1; -
CC EMBL; BC015799; AAH15799.1; -
CC PDB; 1FIJ; 23-MAY-01.
CC PDB; 1GFJ; 04-JAN-02.
CC PDB; 1IAO; 31-OCT-01.
CC PDB; 1I51; 23-FEB-02.
CC PDB; 1K86; 21-NOV-01.
CC PDB; 1K88; 21-NOV-01.
CC PDB; 1KWC; 16-JAN-02.
CC MEROPS; C14.004; -.
CC Genew; HGNC:1508; CASP7.
CC
CC MIM; 601761; -.
CC
CC DR GO; GO:0005737; C:cytoplasm; TAS.
CC DR GO; GO:0008234; F:cysteine-type peptidase activity; TAS.
CC DR GO; GO:0008632; P:apoptotic program; TAS.
CC
CC DR InterPro; IPR002138; ICE p10.
CC DR InterPro; IPR001109; ICE p20.
CC DR InterPro; IPR002398; Peptidase_C14.
CC DR Pfam; PF00656; Peptidase_C14; 1.
CC DR PRINTS; PR00376; ILIBCEZYME.
CC DR SMART; SM00115; CASC; 1.
CC DR PROSITE; PS01122; CASPASE_CYS; 1.
CC DR PROSITE; PS01121; CASPASE_HIS; 1.
CC DR PROSITE; PS0207; CASPASE_P10; 1.
CC DR PROSITE; PS0208; CASPASE_P20; 1.
CC KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
CC 3D-structure.
CC
CC FT PROPEP 1 23
CC FT CHAIN 24 198
CC FT PROPEP 139 206
CC FT CHAIN 207 303
CC FT ACT_SITE 144 144
CC FT ACT_SITE 186 186
CC FT VARSPPLIC 1 1
CC
CC FT VARSPLIC 149 303
CC
CC FT VYIKDGVTPFKDLTAHFRGDRCKTLLKPKLFFTAQCRGT
CC ELDDGIQADSGINDTANPRYKIFVEADFLFAYSTVFGY
CC SWRSPGSGFWALCSILEEHKDLIMQILTRVNDVRAR
CC HPESQSDDPHEHKKQIPCVVSMLTKELYF50 -> MESCS
CC VTQAGVQRDLRLQPPPRLAEGPSLWASRPTGSPMTQ
CC MLILDRTSQWKLTSIPRFOAIRNGAQEAPGLCKFSA
CC PSWRSTKWTGKCRSPG (in isoform Beta).
CC /FTID=VSP 000807.
CC C->A: NO APOPTOTIC ACTIVITY.
CC D -> E (IN REF. 5).
CC G -> A (IN REF. 1).
CC
CC FT MUTAGEN 186 186
CC FT CONFLICT 4 4
CC FT CONFLICT 194 194
CC FT CONFLICT 303 AA; 34276 MW; CD373EB54A232CA4 CRC64;
CC
CC Query Match 16.6%; Score 361.5; DB 1; Length 303;
CC Best Local Similarity 33.3%; Pred. No. 2.6e-23;
CC Matches 92; Conservative 41; Mismatches 94; Indels 49; Gaps 8;
CC
CC 153 YILSMEPOGHCLIIINNVPFCRESGLTRTGSNIDCEKLRRFSSLHFMVYKGLDTAKKM 212
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Db 60 YNNFEKLGKCIINNNKFNDFKVTGMGVNGHDKDAEALFKCFRSLGFDVIVYNDSCAKM 119
Qy 213 VLALLELARQDHGALDCCVVWILSHGCCQASHLPFGAVYGTGCGFVSVEKVNIFNGTSC 272
Db 120 QDLIKKASEEDHTWACFACILLSHGEE-----NVIYKDGVTPIKDLTAHFRGDR 171
Qy 273 PSLGGKPKLFFIACGGSEKQDHGFVEASTSPEDSPGSPNPFDPATFPFQEGRLTFDQDAI 332
Db 172 KTLLEKPKLFFIACRGTELDGIGQADS-----GPINDTDANPRYK----- 212
Qy 333 SSLTPSPDIFVSYSTFPFVSRDPKSGSWVETLDDIFEQWASEDLQ--SLILRVANA 390
Db 213 --IPVEADFLFAYSTVPFGYYSWRSPGRGFWVQALCSILEE--HGKDLIMQILTRVND 268
Qy 391 VS-----VKGIVKQMPGCFNFKKLPFF 413
Db 269 VARHPESQSDDPHFHEK---KQIPCVVSMLTKELYF 301
RESULT 8
ICE7 MOUSE
ID ICE7 MOUSE STANDARD; PRT; 303 AA.
AC P97864; O08669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]_TaxID:10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Wortmannin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Criekeinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci T.L., Scheetz T.E.,
RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
```

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC regulatory element binding proteins (SREBPs). Overexpression
CC promotes programmed cell death (By similarity).
CC -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNIT. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC EMBL; U67321; AAC3068.1; AUT_INIT.
DR EMBL; D86353; BAAL19730.1; -. /
DR EMBL; Y13088; CAA73530.1; -. /
DR EMBL; BC005428; AAH05428.1; -. /
DR HSSP; P42574; 1PAU.
DR MGDI; MGI:109383; Casp7.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZIME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23 BY SIMILARITY.
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
FT CONFLICT 10 11 EL -> DW (IN REF. 2).
FT CONFLICT 45 45 A -> T (IN REF. 2).
FT CONFLICT 48 49 VR -> RQ (IN REF. 2).
SQ SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;

Query Match
Best Local Similarity 16.1%; Score 350.5; DB 1; Length 303;
Matches 88; Conservative 42; Mismatches 100; Indels 43; Gaps 7;
QY 153 YILSLPCHGLIINNVCRESGLRTRGSGIDCEKLRRTSSLSLHFWVEVKGDLTAKM 212
Db 60 YRMDFKMKKCIINNKKFDKATGMDVRNGTDKAGLFCFQNLGFEVTHVNDSCAKM 119
QY 213 VLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDCPVSVSEKIVNIFNGTSC 272

Db 120 QDLRLKASEDSHNSACFACVLISHGE-----DLIYKGV-TEIKDLTAHFRGRC 171
QY 273 PSIGGPKLFFIQACGEGQKHGFVASTSPEDSPGSPNPEPDATPFQEGRTFDQLDAI 332
Db 172 KTLLEKPKLFFIQACRGTELDGIGQADS-----GPINDIDANP-----R 210
QY 333 SLSPTSDIFVSYSTPFGFVSWRDPKSGWYVETLDDIFEQWAHSDLQ--SLLLRVANA 390
Db 211 NKFIVAEADLFAYSTVPGYSWENPGKSWFQALCSILNE--HGKDLIMQILTRVND 268
QY 391 VSVK-----GIYKMPGCGFNLRLKLF 413
Db 269 VARHFESQSDDRFNEKKQIPCMVSLTKELYF 301

RESULT 9
ICE3 XENLA
ID ICE3 XENLA STANDARD; PRT; 282 AA.
AC P55866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3)
DE (CASP-3) (XCPP32).
GN CASP3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[l1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RX MEDLINE=97184166; PubMed=9030578;
RA Yaoita Y., Nakajima K.;
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
RL myoblastic cell line derived from tadpole tail.";
RL J. Biol. Chem. 272:5122-5127(1997)
CC -!- FUNCTION: Important mediator of apoptosis. At the onset of
CC apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase
CC (PARP) at a 216-Asp-Gly-217 bond (By similarity).
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12)
CC subunits.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The subunits are derived from the precursor
CC sequence by a probable autocatalytic mechanism and probably by
CC other caspases (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D89784; BAAL4018.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZIME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 186 BY SIMILARITY.
FT CHAIN 2 186 APOPAIN P17 SUBUNIT.

Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapienson M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*.";
Science 287:2185-2195(2000).
[3]
SEQUENCE FROM N.A.
RP STRAIN=Berkeley; TISSUE=Head;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A *Drosophila* full-length cDNA resource.";
RLL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Acts downstream of rpr.
CC Cleaves baculovirus p35 and lamin Dmo in vitro.
CC -!- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
CC -!- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
CC occurs.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC or send an email to license@isb-sib.ch.
CC
CC EMBL; Y12261; CAAY72937.1; -;
DR EMBL; A5003771; AAF569319.1; -;
DR EMBL; AY058451; AAL13680.1; -;
DR HSPRP; P42574; 1PAU.
DR MEROPS; C14.015; -;
DR FlyBase; FBgn0019972; Ice.
DR GO; GO:0004207; F.effector caspase activity; NAS.
DR GO; GO:0006915; P.apoptosis; NAS.
DR InterPro; IPR002138; ICE.p10.
DR InterPro; IPR001309; ICE.p20.
DR Pfam; PF00656; Peptidase C14.
DR PRINTS; PR00376; ILLBENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1 28
FT CHAIN 29 217 BY SIMILARITY.
FT PROPEP 218 230 CASPASE SUBUNIT P21 (BY SIMILARITY).
FT CHAIN 231 339 BY SIMILARITY.
FT ACT_SITE 169 169 CASPASE SUBUNIT P12 (BY SIMILARITY).
FT ACT_SITE 211 211 BY SIMILARITY.
FT CONFLICT 151 151 A -> S (IN REF. 1).
FT CONFLICT 265 265 S -> T (IN REF. 1).
FT

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SQ SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;
Query Match 14.8%; Score 324; DB 1; Length 339;
Best Local Similarity 29.0%; Pred. No. 4.7e-20;
Matches 90; Conservative 37; Mismatches 123; Indels 60; Gaps 6;

QY 115 IRKPEVLRETPRPVDVIGSGGQDVCAL-----ESLRGNA-- 149
D 17 VGNPEQNDHTDALGVSQGGAGSGGLVAGSHYPSGGAIGLANGYSSPSSYRKNVAK 76
QY 150 -----DLAYILSMPCGCHLIINNVCRESGLRTRGTSNIDCEKLRFRFSLHFMVEV 203
D 77 MYTDRHAEYNNRKNRGWALFNHEHF-EVTLKSRAGTNDNCNLTFLVKQLDFEVTV 135
QY 204 KGLTAKMVLALLEARHDGALDCVVLVILSHGCOASHLQPPGAVYGTDCGVSVEKI 263
D 136 YKDCRYKDLRTIEVAASQNSHSDCILVAILLSHGEM-----GYIYAKD-TQYKLDNI 187
QY 264 VNIENGTSCPSLGGKPKLFFIOACGGEQKHGFVASTSPEDSPGSPNPEPDATPQEG 323
D 188 WSEFTANHCPSLAGPKLFFIOACQGRDLDGGVTWQRTOTETDGDSS----- 234
QY 324 RTFDQDAISSLFTSPDIPVSYSTFPFGVSWRDPKSGSWYVETLDDIFQWHAHSDLOSL 383
D 235 -----MSYKIPVHADFLLIAYSTVPGFYSWRTTGSWFMQSLCAELAANGKRLDILTL 287
QY 384 LLRVANAVSV 393
D 288 LTFVCQVAV 297

RESULT 11
ICE6_MOUSE STANDARD; PRT; 276 AA.
AC 008738;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Leeuwen G., Molenans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death (By similarity).
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
CC testis, and heart. Lower levels in spleen, skeletal muscle and
CC brain.
CC -!- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC EMBL; Y13087; CAA73529.1; -.
DR HSP; P42574; LPAU.
DR MEROPS; C14.005; -.
DR MGD; MGI:1312921; Casp6.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASP; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 5
FT CHAIN 6 162 CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
FT PROPEP 163 176 BY SIMILARITY.
FT CHAIN 177 276 CASPASE-6 SUBUNIT P11 (BY SIMILARITY).
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 276 AA; 31595 MW; 5665DE932112686C CRC64;

Query Match 14.8%; Score 322; DB 1; Length 276;
Best Local Similarity 33.1%; Pred. No. 5.2e-20;
Matches 88; Conservative 39; Mismatches 103; Indels 36; Gaps 9;

QY 161 GHCLINNVNFCRESGLRTRGTSNIDCEKLRFRFSLHFMVEVKGDLTAKMVLALLEA 220
D 28 GVALLFNHERFFWHLTPERRGTNADRLNTRFSDGLGFVKCFNDRAEELLKHEVS 87
QY 221 QDGHGALDCVVLVILSHGCOASHLQPPGAVYGTDCGVSVEKIVNIENGTSCPSLGGKPK 280
D 88 TSSHIDADCFCVFLSHG-EGNH-----VYAYD-AKIEITLTGLFGDKCQSLVGKPK 139
QY 281 LFFTOACGGEQKHGFVASTSPEDSPGSPNPEPDATPQEGRLTFDQDAIS--SLPTP 338
D 140 IFIICAKGSGQ--HDVPVPLDMVDHQ-----TDKLDNVTQVDAASVVTLPAG 185
QY 339 SDFVSVSTFPFGVSWRDPKSGSWYVETLDDIFQWHAHSDLOSLLLRVANAVSVKGI-- 396
D 186 ADFLMCVSAEGYSHRETVNGSWYIQDCEMLARYSGSLEFTELLTLVNRKVSRRVDF 245
QY 397 -----YKOMPQGF-NFLRKLFF 413
D 246 CKDPDAIGKKQVP-CFASMLTKLHF 270

RESULT 12
ICE1_DROME STANDARD; PRT; 323 AA.
ID ICE1_DROME
AC 002002; OSW1N0;
DT 15-JUL-1998 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-).
GN DCP-1 OR CG5370.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.
RC TISSUE=Embryo;
RX MEDLINE=97153052; PubMed=899799;
RA Song Z., McCall K., Steller H.;
RT "DCP-1, a Drosophila cell death protease essential for development.";
RL Science 275:536-540(1997).
RN [2]
RP ERRATUM.
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Song Z., McCall K., Steller H.;
Science 277:167-167(1997).
[3]
SEQUENCE FROM N.A.
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berwan B.P., Bhargava D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
[4]
SEQUENCE FROM N.A.
STRAIN=Berkeley; TISSUE=Embryo;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W., E.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Fafan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
RA Miranda A., Mungall C.J., Munoz J., Pacleb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.E.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution (By similarity).
CC Proteolytically cleaves poly(ADP-ribose) polymerase (PARP). Loss
CC of zygotic DCP-1 function causes larval lethality and melanotic
CC tumors.
CC -!- SUBUNIT: Heterodimer of a 22 kDa (p22) and a 13 kDa (p13) subunit.
CC -!- DEVELOPMENTAL STAGE: Present uniformly throughout embryos of
CC stages 4 and 10. In stage 16 embryos, the expression becomes
CC restricted to the central nervous system, the developing gonads,
CC and a portion of the gut. In stage 17 embryos, expression is
CC mainly localized in cells along the midline of the central nervous
CC system.
CC -!- SIMILARITY: Belongs to peptidase family C14.

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CC purposes is prohibited.

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
PROCESSING.
TISSUE=Lymphocytes;
MEDLINE=97059171; PubMed=890201;
RA Strinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
RT mediator CPP32.";
RT J. Biol. Chem. 271:27099-27106(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=P55212-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P55212-2; Sequence=VSP_000805;
CC -!- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U20536; AAC50168.1; -;
CC EMBL; U20537; AAC50169.1; -;
CC EMBL; AY254046; AA063494.1; -;
CC EMBL; BC000305; AA00305.1; -;
CC EMBL; BC004460; AA04460.1; -;
CC HSSP; P42574; LPAU.
CC MEROPS; C14.005; -;
CC Genes; HGNC:1507; CASP6.
CC MIM; 601532; -;
CC GO; GO:0008234; P:cysteine-type peptidase activity; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC InterPro; IPR002398; Peptidase C14.
CC Pfam; PF00656; Peptidase C14; 1.
CC PRINTS; PR00376; ILIBCEZYME.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS50207; CASPASE_P10; 1.
CC PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing;
KW Polymorphism.
FT PROPEP 1 23
FT CHAIN 24 179 CASPASE-6 SUBUNIT P18.
FT PROPEP 180 193
FT CHAIN 194 293 CASPASE-6 SUBUNIT P11.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT VARSPIC 14 102 Missing (in isoform Beta).
FT VARIANT 109 109 A -> T (in dbSNP:5030674).
FT CONFLICT 66 66 G -> R (in REF. 1).
FT SEQUENCE 293 AA; 33310 MW; 0738AE4F9791EBD7 CRC64;

Query Match 14.3%; Score 311.5; DB 1; Length 293;
Best Local Similarity 32.3%; Pred. No. 4.4e-19;
Matches 86; Conservative 40; Mismatches 105; Indels 35; Gaps 9;

QY 161 GHCLINNNVFCRESGLRTGTSNIDCEKLRFRFSSLHPFVVKGDLTKAKMYLALLELA 220
Db 45 GTALINNNHRRFFWHLTPERRGTGTCADRDNLTRFSDLGFEVKCFNDLKAEELLKTHEVS 104
QY 221 RQDHGALDCVVVILSHGQASHLQFPGAVYGTGCPVSVEKIVNIPNGTSCPSLGGKPK 280
Db 105 TVSHADADCFVCVFLSHG-EGNH-----IYAYD-AKIEIQTLTGLFKGDKCHSLVGGPK 156
QY 281 LPIQACGGEQKHGFEVASTSPEDSPGSPNPDPATPFQEGRLTFDQDAIS--SLPTP 338
Db 157 IFIIQACRGQHD-----VPIPLDVVDNQTEKLDT-----NITEVDAASVYTLDPAG 203
QY 339 SDIFVSYSFPGFVSWRDPKSGSWYVETLDDIIEQMAHSDQLQSLLRVANAVSVKGI-- 396
Db 204 ADFLMCYSAEGYSHRETVNGSWYIQDLCMLGKYSSLEFTELLTLVNRKYSQRVDF 263
QY 397 -----YKMPGCP-NFLRKXKLF 413
Db 264 CKDPSAIGKKQVP-CFASMLTKKLHF 288

RESULT 15

IIIC HORSE
ID IIIC HORSE STANDARD; PRT; 405 AA.
AC Q9TVL3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase precursor (IL-1BC) (EC 3.4.22.36) (IL-1
DE beta converting enzyme) (ICE) (interleukin-1 beta converting enzyme)
DE (P45) (Caspase-1) (CASP-1).
DE CASP1 OR IL1BC.
GN Equus caballus (Horse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9304505; PubMed=10376217;
RA Wardlaw S., Penha-Goncalves M.N., Argyle D.J., Onions D.E.,
RA Nicolson L.;
RT "Nucleotide sequence of equine caspase-1 cDNA.";
RL DNA Seq. 10:133-137(1999).
CC -!- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and
CC an Ala, releasing the mature cytokine which is involved in a
CC variety of inflammatory processes (By similarity).
CC -!- CATALYTIC ACTIVITY: Release of interleukin 1-beta by specific
CC cleavage at 116-Asp--|Ala-117 and 27-Asp--|Gly-28 bonds in
CC precursor. Also hydrolyzes the small-molecule substrate, Ac-Tyr-
CC Val-Ala-Asp--|NHMe.
CC -!- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa
CC (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a
CC heterodimer with the epsilon isoform which then has an inhibitory
CC effect (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: The two subunits are derived from the precursor sequence by
CC an autocatalytic mechanism.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; AF090119; AAD46400.1; -;

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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:58:51 ; Search time 39 Seconds
(without alignments)
3365.527 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCFNFKLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 789523

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 416

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	61.3	393	11 Q9R0S9	Q9R0S9 mus musculus
2	1093	50.1	383	11 Q99M88	Q99M88 rattus norv
3	1048.5	48.1	399	13 Q91B63	Q91B63 xenopus lae
4	1000.5	45.9	403	13 Q90WU0	Q90WU0 gallus gall
5	613	28.1	229	11 Q7TQC1	Q7TQC1 rattus norv
6	485	22.2	177	11 Q92UG4	Q92UG4 rattus norv
7	437	20.0	313	11 Q8CHV5	Q8CHV5 mus musculus
8	435	20.0	316	5 Q817B0	Q817B0 geodia cydo
9	421	19.3	328	5 Q81TP3	Q81TP3 branchiosto
10	420	19.3	277	6 Q95ND5	Q95ND5 sus scrofa
11	419	19.2	277	6 Q8MJU1	Q8MJU1 felis silve
12	418	19.2	280	13 Q8JGM9	Q8JGM9 fugu rubrip
13	413	18.9	280	13 Q8JG42	Q8JG42 fugu rubrip
14	402.5	18.5	318	13 Q91B65	Q91B65 xenopus lae
15	401	18.4	277	6 Q8MK15	Q8MK15 canis famil
16	401	18.4	277	6 Q8MJC3	Q8MJC3 oryctolagus

ALIGNMENTS

RESULT 1

Q9R0S9	PRELIMINARY;	PRT;	393 AA.
ID	Q9R0S9		
AC	Q9R0S9;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Caspase9S.		
GN	CASP9.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20001956; PubMed=10529400;		
RA	Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;		
RT	"Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9."		
RL	Biochem. Biophys. Res. Commun. 264:550-555 (1999).		
DR	EMBL; AB019601; BAA86896.1; -		
DR	HSSP; P42574; IPAU.		
DR	MEROPS; C14.010; -		
DR	MGD; MGI:1277950; Casp9.		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.		
DR	GO; GO:0030693; F:caspase activity; IEA.		
DR	GO; GO:0006915; P:apoptosis; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001315; CARD.		
DR	InterPro; IPR001309; ICE.p20.		
DR	InterPro; IPR002398; Peptidase_C14.		
DR	Pfam; PF00619; CARD; 1.		
DR	Pfam; PF00656; Peptidase_C14; 1.		
DR	PRINTS; PR00376; ILLBCEZYME.		
DR	SMART; SM00114; CARD; 1.		
DR	SMART; SM00115; CASC; 1.		
DR	PROSITE; PS0209; CARD; 1.		
DR	PROSITE; PS01122; CASPASE_CVS; 1.		

Q93417 gallus gall
Q98ui8 brachydanio
Q8jis9 oryzias lat
Q8jis8 oryzias lat
Q80im6 xenopus lae
Q88550 rattus norv
O77623 ovis aries
Q86f10 anopheles s
Q8itp2 branchiosto
Q93415 gallus gall
Q99m47 mus musculu
Q9d889 mus musculu
Q91b66 xenopus lae
Q8bnt4 mus musculu
Q35397 rattus norv
Q9gv88 hydra atten
Q9wui6 rattus norv
Q86u33 homo sapien
Q819v7 bombyx mori
Q81955 spodoptera
Q918s9 oncorhynchu
Q9v89 drosophila
Q9nhf9 drosophila
Q8k4i9 meriones un
Q91w32 rattus norv
Q9tzb5 caenorhabdi
Q91917 brachydanio
Q9gv89 hydra atten
Q9tzb6 caenorhabdi

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DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
SQ SEQUENCE 393 AA; 42975 MW; CA889475B50DD632 CRC64;

Query Match
Best Local Similarity 61.3%; Score 1336; DB 11; Length 393;
Matches 267; Conservative 26; Mismatches 57; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQAGSGRRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQAGSGRRDQARQLV 60
QY 61 DLETRGSAALPLFISCLDGTGDMLASFLRTNRQAGKL----- 98
DB 61 DLETRGSAALPLFISCLDGTGDMLASFLRTNRQAGKL----- 98
QY 99 -----SKPTLENLTTPVLRPE-----IRKPEVLRPETPRPVDIGSGGFGDVGAL 120
DB 121 AKEQKRVKLETSQPAVGNLTTPVVLGPEELWPARKPEVLRPETPRPVDIGSGGADVCP 180
QY 143 ESLRGNADLAYILSMPCGHCLIIINNVCRESGLRTRTGNIDCEKLRRLRPSLHFVWE 202
DB 181 GKIRHADWAYTLDSDPCGHCLIIINNVCRESGLRTRTGNIDCEKLRRLRPSLHFVWE 240
QY 203 VKGDLTAKKMWLALMLARQDHGALDCCVVVILSHGCCOASHLOFFGAVYGTDCGCPVSVEK 262
DB 241 VKNDLTAKKMWYALMEMAHNRHLDCCFVVVILSHGCCOASHLOFFGAVYGTDCGCSVIEK 300
QY 263 IVNIFNGTSCPSLGGKPKLFFTIQACGGKQKHGFVASTSPEDSGNBPDPATPFQEG 322
DB 301 IVNIFNGTSCPSLGGKPKLFFTIQACGGKQKHGFVASTSPEDSGNBPDPATPFQEG 360
QY 323 LRTFDLDAISLTPSDFVSYSTFP 350
DB 361 PRPLDQDAVSSLPSTPSDILVSYSTFP 388

RESULT 2
Q99M88 PRELIMINARY; PRT; 383 AA.
AC Q99M88;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Caspase-9 CTD isoform.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RT Apoptosis.";
RL J. Biol. Chem. 276:12190-12200(2001).
DR EMBL; AY08275; AAG21690.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBENZIME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.

RESULT 3
Q9IB63 PRELIMINARY; PRT; 399 AA.
AC Q9IB63;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBENZIME.
DR SMART; SM00114; CARD; 1.
DR SMART; PR00376; ILIBENZIME.
```

DR SMART; SM00114; CARD; 1.
DR PROSITE; PS00209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02007; CASPASE_P10; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
SQ SEQUENCE 399 AA; 4772 MW; E2A269719064F9F CRC64;

Query Match 48.1%; Score 1048.5; DB 13; Length 399;
Best Local Similarity 51.8%; Pred. No. 1.5e-85;
Matches 216; Conservative 67; Mismatches 113; Indels 21; Gaps 6;

QY 1 MDEADRLRLCRRLVVELOVDQMLVLSRELPRPHMIEDIQAGSGRRDQARLI 60
DB 1 MEQELRDILRRNRVLVSQVKEUWDLVVERGVFSNDMIEIQR--EGTRDQARKLLV 58

QY 61 DLETRGSQLPLFISCLDGTGDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
DB 59 ELETGSGQAFPLFLCLKETAQHDADFLQSD--SGTRVLQPIPTTSP--VLKP---LPKA 113

QY 121 LRPEPRPVDSIGSGFVDGVALESRG--NADLAVILSWPCGHCLINNVNFCRESGLR 178
DB 114 EPAEYF-----AREIRSRKGLDKDYPMSDDPIGFCLLINNMNPFECTGLS 161

QY 179 TETGSDICEKLRFRSSLSHFVVKGLDTAKKWLALLELARQDHGALDCCVWVILSHG 238
DB 162 TETGSDIDRDKLANRMSPHFEVTVKNDLUTGQMDHDLQALADQDHSQDCLVILSHG 221

QY 239 COASHLQFPAGVYGTGCPVSVEKIVNIENGTSCEPSLGGKPKLFFIAQCGGQKHGFV 298
DB 222 CETHRIQFPGVYGTGIRIPVERIVSYFNGSKPSLRGKPKIFIAQCGGQKHGCEV 281

QY 299 ASTSPDESPGNPEPDATPFQEGLTFTQDLAISLPTSPSIFVSYSTFPFVSVSRDPK 358
DB 282 TSETPLPSLTSQSDATPFVSGEGDRVDAVSNIPSPSILVSYSTFPFVSVSRDKH 341

QY 359 SGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSVGIYKOMPFCNFKKLFFKFT 415
DB 342 TGSWYVEVLDVLAEEHAAADDDLSLLVWADGVSSKGYKQIFGYFNFLKRYFKT 398

RESULT 4
Q90WU0 PRELIMINARY; PRT; 403 AA.
ID Q90WU0
AC Q90WU0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgman J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02007; CASPASE_P10; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
FT NON TER 1
SQ SEQUENCE 403 AA; 4913 MW; 0F1E40C3E6594FC4 CRC64;

Query Match 45.9%; Score 1000.5; DB 13; Length 403;
Best Local Similarity 55.3%; Pred. No. 3.1e-81;
Matches 208; Conservative 45; Mismatches 100; Indels 23; Gaps 7;

QY 52 RDOARQLIIDLETRGSQLPLFISCLDGTGDMLASFLRTNRQAGKLSKPTLENLTPVVL 111
DB 34 KEQARQLVIDLETRGSQLPLFISCLDGTGDMLASFLRTNRQAGKLSKPTLENLTPVVL 90

QY 112 R-PEIRKPE-----VLRPEPR---PVDIGSGFVDGVALESRLGNADLAILSM 157
DB 91 ELPGRDRKDSYSTAERLSIPVQESERFMPPEPAQG-----SAVDKSR--PTDWTSCBQ 144

QY 158 EPCGHCLINNVNFCRESGLRTRTGSNDICEKLRFRSSLSHFVVKGLDTAKKWLALL 217
DB 145 TPCGHCLIFNNVFSFRSDLSSTRAGSDIDCEKLRFRSSLSHFVVKGLDTAKKWLALL 204

QY 218 ELARODHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVEKIVNIENGTSCEPSLGG 277
DB 205 KUARDHSGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVEKIVNIENGTSCEPSLGG 264

QY 278 KPKLFFIAQCGGQKHGFVASTSPDESPOGNSPEPDATPFQEGLTFTQDLAISLPT 337
DB 265 KPKLFFIAQCGGQKHGFVASTSPDESPOGNSPEPDATPFQEGLTFTQDLAISLPT 324

QY 338 PSDIFVSYSTFPFVSVSRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSVGIY 397
DB 325 PGDILVSYSTFPFVSVSRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSVGIY 384

QY 398 KQMGCCFNFLKRLFF 413
DB 385 KQIPGCFNFLKRLFF 400

RESULT 5
Q7TQCI PRELIMINARY; PRT; 229 AA.
ID Q7TQCI
AC Q7TQCI
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 25 kDa caspase-9 dominant negative protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Wu S., Sheng L., Graham S.H., Zhou Z., Chen J.;
RT "Molecular cloning and characterization of three caspase-9 dominant
RT negative forms in rats";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY124461; AAM92272.1; -
SQ SEQUENCE 229 AA; 25194 MW; 87C293AF139F3B23 CRC64;

Query Match 28.1%; Score 613; DB 11; Length 229;
Best Local Similarity 59.7%; Pred. No. 9.1e-47;
Matches 132; Conservative 14; Mismatches 37; Indels 38; Gaps 2;

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QY 1 MDEADRLRLRCRLRLVVEELQVDLWDVLLSRELFRPHMIEDIQAGSGRRDQAROLII 60
Db 1 MEEADQLRLRCRLRLVVEELQVAELWDGLLSRELFTDMIEDIQAGSGRRDQAROLVI 60
QY 61 DLETRGSOALPLFISCLDTGQDMLASFLRTNRQAGL----- 98
Db 61 DLETRGSOALPLFISCLDTGQDMLASFLRTNRQAGL----- 98
QY 99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRLPETERPVDIGSGGFGDVGAL 120
Db 121 SKEQKVVLDPSPALGNLTPVVLGPEELWPTLRPEVLTPETPRPVDIGSGRAHDVCTP 180
QY 143 ESLRGADLAYILSWPEPOGHCLIIINNVCRESGLRTRGS 183
Db 181 GKIERHADWAYTLDSDCGHCPIINNVCPCSSGLSTRIGS 221

RESULT 6
Q920G4
ID Q920G4 PRELIMINARY; PRT; 177 AA.
AC Q920G4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Caspase-9 short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1
SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
CAO G., Chen D., Ma L., Graham S.H., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293333; AAK97086.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS02029; CARD; 1.
SQ SEQUENCE 177 AA; 19700 MW; E9DCDA77156AD748 CRC64;

Query Match 22.2%; Score 485; DB 11; Length 177;
Best Local Similarity 60.5%; Pred. No. 2e-35;
Matches 107; Conservative 10; Mismatches 22; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVVEELQVDLWDVLLSRELFRPHMIEDIQAGSGRRDQAROLII 60
Db 1 MEEADQLRLRCRLRLVVEELQVAELWDGLLSRELFTDMIEDIQAGSGRRDQAROLVI 60
QY 61 DLETRGSOALPLFISCLDTGQDMLASFLRTNRQAGL----- 98
Db 61 DLETRGSOALPLFISCLDTGQDMLASFLRTNRQAGL----- 98
QY 99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRLPETERPVDIGSGGFGDV 139
Db 121 SKEQKVVLDPSPALGNLTPVVLGPEELWPTLRPEVLTPETPRPVDIGSGRAHDV 177

RESULT 7
Q8CHV5
ID Q8CHV5 PRELIMINARY; PRT; 313 AA.
AC Q8CHV5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase 3, apoptosis related cysteine protease (Fragment).
GN CASP3.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
SEQUENCE FROM N.A.
RA STRAIN=FVB/N;
CA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038825; AAH38825.1; -.
DR MGD; MGI:107739; Casp3.
DR GO; GO:0003693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Protease.
FT NON_TER
SQ SEQUENCE 313 AA; 35174 MW; 96E98A1F04E769FC CRC64;

Query Match 20.0%; Score 437; DB 11; Length 313;
Best Local Similarity 31.5%; Pred. No. 9.1e-31;
Matches 106; Conservative 52; Mismatches 123; Indels 56; Gaps 5;

QY 87 SFLTNQAGKLSKPTLENTTPVVLRLPEIRKPEVLRLPETERPVDIGSGGFGDVGALSLR 146
Db 21 SVLRGAWNGTLRKVTMNNKTSVDSKSIINNFEVKTTHGSKSVDSGI----- 67
QY 147 GNADLAYILSWPEPCGHCLIIINNVCRESGLRTRTGSNIDCEKLRFRPSSLHFVVEKGD 206
Db 68 -YLDSSYKMDYPENGICIIINNKNFKSTGMSRSGTDVAANLRETFMGLKYQVRNKND 126
QY 207 LTAKMVLALLELARQDHGALDCCVVVLSHGQASHLPFGVAVYGTDCGCPVSEKIVNI 266
Db 127 LTREDILLELMDSVSKEDHSKRSFVCLSHGDE-----GVYIYNG-PVELKULTSF 178
QY 267 FNGTSPSLGCKPKLFFIQACGGEQKHGFEVASTSPEDSPGSNPFDPATPFQEGLTRF 326
Db 179 FRGDYCRSLTGKPKLFFIQACRGTELDGCTETDSTGDE----- 218
QY 327 DQLDAISSLTPSPDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLR 386
Db 219 ----ACQKIPVEADFLYAVSTAGFYYSWRNSKDGSMFIQSLCSMLKLYAHKLFEMHLTR 274
QY 387 VANAVSVK-----GIYKMPGCGFNFLRKKLFF 413
Db 275 VNRKVATEFESFLDSTFHAQKQIPCVSMLTKELYP 311

RESULT 8
Q8I7B0
ID Q8I7B0 PRELIMINARY; PRT; 316 AA.
AC Q8I7B0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase 3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN 1
SEQUENCE FROM N.A.
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function."

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[illegible]

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Db 34 DVSYKMDYFENGGLCIINNNKFKDKMGWACSGTGDVDAANLRETFTNLKYEVRNKDLTR 93
QY 210 KMWLALLELARQDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGCPVSVKIVNIFNG 269
Db 94 BEILLEMHVSKEKSHKSSKSSFCVLLSHGEE-----GKIFGNG-PVDLKKLTSPFRG 145
QY 270 TSCPSLGGKPKLFFIOACGCGEKDGHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQL 329
Db 146 DCCRTLTGKPKLFFIOACRGTELDGCIETDSTGTEDDM----- 182
QY 330 DAISLPTSPDIFVSYSTPFGVSWRDPKSGSVVETLDDIFEQWAHSEDLOSLLLRVAN 389
Db 183 -ACQKIPVEADFLYAYSTAGYYSWRNSKDGSWFIQSLCAALKOYVHKELMHILTRVNR 241
QY 390 AVSVK-----GIYKMPGCFNFKLFF 413
Db 242 KVAVEFESFTDSTFHAQKQICIVSMILTKELF 275

RESULT 11
Q8JMU1 PRELIMINARY; PRT; 277 AA.
AC Q8JMU1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Caspase3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RF SEQUENCE FROM N.A.
RA Yamazaki J., Sano J., Kano R., Hasegawa A.;
RT "Felis catus mRNA for caspase3, complete cds.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB030246; BAC10589.1;
GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR002138; ICE_p10.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SMO0115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;

Query Match 19.2%; Score 419; DB 6; Length 277;
Best Local Similarity 33.6%; Pred. No. 3.2e-29;
Matches 92; Conservative 49; Mismatches 91; Indels 42; Gaps 5;

QY 150 DLAYLSMPCGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHFMVVKGLTAKM 209
Db 34 DNSYKMDYFENGGLCIINNNKFKDKMGWACSGTGDVDAANLRETFTNLKYEVRNKDLTR 93
QY 210 KMWLALLELARQDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGCPVSVKIVNIFNG 269
Db 94 EQIVALLDSVSRSHKSSKSSFCVLLSHGEE-----GLIYFNG-PVDLKKLTGFFRG 145
QY 270 TSCPSLGGKPKLFFIOACGCGEKDGHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQL 329
Db 146 DCCRTLTGKPKLFFIOACRGTELDGCIETDSTGTEDDM----- 181
QY 330 DAISLPTSPDIFVSYSTPFGVSWRDPKSGSVVETLDDIFEQWAHSEDLOSLLLRVAN 389
Db 182 IACQKIPVEADFLYAYSTAGYYSWRNSKDGSWFIQSLCSMLRLYAHLEFHMILTRVNR 241
QY 390 AV-----SVKGIY---KQMPGCFNFKLFF 413

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Db 242 KVATEFESFLDSAFHGKQKQICIVSMILTKELF 275

RESULT 12
Q8JGM9 PRELIMINARY; PRT; 280 AA.
AC Q8JGM9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3-like.
GN CASP3
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RF SEQUENCE FROM N.A.
RA Hewitt J.E., Bolland D.J.;
RT "Sequence comparisons of an evolutionary chromosomal breakpoint in human, mouse and pufferfish.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY102865; AAM48291.1;
GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SMO0115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
SQ SEQUENCE 280 AA; 30538 MW; 4D58912159A37347 CRC64;

Query Match 19.2%; Score 418; DB 13; Length 280;
Best Local Similarity 33.9%; Pred. No. 4e-29;
Matches 92; Conservative 44; Mismatches 91; Indels 44; Gaps 4;

QY 153 YILSMPCGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHFMVVKGLTAKM 212
Db 43 YSLDFPNMGHCIIINNNKFKDKMGWACSGTGDVDAANLRETFTNLKYEVRNKDLTR 102
QY 213 VLALLELARQDHGALDCCVVILSHGCOASHLQFPGAVYGTDCGCPVSVKIVNIFNGTSC 272
Db 103 KQLLSAAEEDHSAACAFVCLLSHGDE-----GVFFGTG-SVELKYLTSIFRGDRC 154
QY 273 PSLGGKPKLFFIOACGCGEKDGHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQDAI 332
Db 155 KSLVGKPKLFFIOACRGNDLGGIETDAA-----SST 188
QY 333 SLSLPTSPDIFVSYSTPFGVSWRDPKSGSVVETLDDIFEQWAHSEDLOSLLLRVANYS 392
Db 189 TKIPVEADFLYAYSTAGYYSWRNTTSGSWFMSQSLDAISKYKKELELOHILTRVNHKA 248
QY 393 VK-----GIYKMPGCFNFKLFF 413
Db 249 VDFESVSNLPGFDAKKQKQICIVSMILTKELF 279

RESULT 13
Q8JG42 PRELIMINARY; PRT; 280 AA.
AC Q8JG42
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Caspase 3.

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Db 249 VDFESVNLPGFADAKQIPCIIVSMITKEMVF 279

RESULT 14

Q9IB65 PRELIMINARY; PRT; 318 AA.

ID Q9IB65

AC Q9IB65, TREMBLrel. 15, Created

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 25, Last annotation update)

DE Caspase-7.

GN XCASPASE-7.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209426; PubMed=10744739;

RA Nakajima K., Takahashi A., Yaoita Y.;

RT "Structure, expression and function of the Xenopus laevis caspase

RT family.";

RL J. Biol. Chem. 275:10484-10491(2000).

DR EMBL; AB038170; BAA94748.1; -.

DR HSSP; P42574; 1PAU.

DR MEROPS; C14.004; -.

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE.p10.

DR InterPro; IPR001309; ICE.p20.

DR InterPro; IPR002398; Peptidase.C14.

DR Pfam; PF00656; Peptidase.C14; 1.

DR PRINTS; PR00376; ILIBCENZYME.

DR SMART; SM00115; CASc; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS02027; CASPASE_P10; 1.

DR PROSITE; PS02028; CASPASE_P20; 1.

SQ SEQUENCE 318 AA; 35937 MW; 6EB06684AF86A128 CRC64;

Query Match 18.5%; Score 402.5; DB 13; Length 318;

Best Local Similarity 30.4%; Pred. No. 1.2e-27;

Matches 106; Conservative 54; Mismatches 124; Indels 65; Gaps 8;

QY 78 EDTQDMLASPLRTNRQAGKLSKETLENLTFVWLRPELRKPEVLRPETPRPVDIGSGGFG 137

Db 23 EEEGEDSV-----AKPDRSQRFISSTKKKKVEDPKPKNNNRVITPAF- 69

QY 138 DVGALESIRGNADLAYILSMPEPCGHCLIIINNVNFCRESGLRTRTGSNIDCEKLRFRSSL 197

Db 70 -----QYKNNNGVGRCIINNKIPDKITGMGRNGTDDARELLRCFKGL 115

QY 198 HFVVEVKGDLTAKKMLLALALRQDHGALDCCVVVILSHGQASHLOFPAGAVYTDGC- 256

Db 116 GFDVNVYNNKSCSEENLRLTVAQDHKDSACFACIFLSHGEE-----GLIYGTGAM 168

QY 257 PVSVEKIVNIINGTSCPSLGGKPKLFFTOACGGEQKHGFVASTSPESPGSNPEPDA 316

Db 169 PIKV--LTLTFRGDCNCRSLVGGPKLFFTOACGHEFFDGLDAGDSVND-----SLETD 221

QY 317 TFFQGLRFTDQDAISSIPTSDIFVSYSSTPPGFVSRDPKSGSWYVETLDDIFEQWAH 376

Db 222 NFRHK-----IPVEADFLYAYSTVPGYYSWRNPGMSWFWQALCSVLNEYK 268

QY 377 SEDLOSLLLRVANAVSVK-----GIYKMPGCFNFKKLPFKT 415

Db 269 ELEVMQILTRVFLVATQFESYSDDPQFSKKQIPCVSMITKELYFS 317

RESULT 15

Q8MK15 PRELIMINARY; PRT; 277 AA.

ID Q8MK15

GN CASP3.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97311173; PubMed=9166581;

RA Grewal P.K., van Deutekom J.C., Mills K.A., Lemmers R.J.,

RA Mathews K.D., Frants R.R., Hewitt J.E.;

RT "The mouse homolog of FRGL, a candidate gene for FSHD, maps proximal

RT to the myodysplasia mutation on chromosome 8.";

RL Mamm. Genome 8:394-398(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98382568; PubMed=9714712;

RA Grewal P.K., Todd L.C., van der Maarel S., Frants R.R., Hewitt J.E.;

RT "FRGL, a gene in the FSH muscular dystrophy region on human chromosome

RT 4q35, is highly conserved in vertebrates and invertebrates.";

RL Gene 216:13-19(1998).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21303262; PubMed=11410364;

RA Bolland D.J., Hewitt J.E.;

RT "Intron loss in the SART1 genes of Fugu rubripes and Tetraodon

RT nigroviridis.";

RL Gene 271:43-49(2001).

RN [4]

RP SEQUENCE FROM N.A.

RA Bolland D.J., van Geel M., Carim Todd L., Grewal P.K., Beck A.F.,

RA van der Maarel M. Sr., Frants R.R., de Jong P.J., Hewitt J.E.;

RT "Sequence Comparisons of an Evolutionary Chromosomal Breakpoint in

RT Human, Mouse and Puffer Fish.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF042797; AA043816.1; -.

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001309; ICE.p10.

DR InterPro; IPR002398; Peptidase.C14.

DR Pfam; PF00656; Peptidase.C14; 1.

DR PRINTS; PR00376; ILIBCENZYME.

DR SMART; SM00115; CASc; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS02027; CASPASE_P10; 1.

DR PROSITE; PS02028; CASPASE_P20; 1.

SQ SEQUENCE 280 AA; 30524 MW; 4F2D91245A7EC642 CRC64;

Query Match 18.9%; Score 413; DB 13; Length 280;

Best Local Similarity 33.6%; Pred. No. 1.1e-28;

Matches 91; Conservative 44; Mismatches 92; Indels 44; Gaps 4;

QY 153 YLLSEPCGHCLIIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKM 212

Db 43 YSLDFPNMGHCIIINNKIPDRGTGMNRTGTVDAANAKVFLSLGKVKVHNDQTVNQM 102

QY 213 VLALLELARQDHGALDCCVVVILSHGQASHLOFPAGAVYTDGCPVSVKEKIVNIINGTSC 272

Db 103 KQLIVSAEEDHSACSFVCLLSHGDE-----GVFFGTG-SVELKYLTLFRGDR 154

QY 273 PSLGGKPKLFFTOACGGEQKHGFVASTSPESPGSNPEPDATEFFQGLRFTDQDAI 332

Db 155 KSLVGRKPKLFFTOACRGNLDGGIETDSAAD-----SST 188

QY 333 SSLPTSDIFVSYSTPPGFVSRDPKSGSWYVETLDDIFEQWAHSEDLOSLLLRVANAVS 392

Db 189 TKIPVEADFLYAFSTAPGYYSWRNTSGSWFMQSLDCAISKYKELEQLHILTRVNHKVA 248

QY 393 VK-----GIYKMPGCFNFKKLPFF 413

```

AC Q8MK15;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Sano J.;
RT "canine caspase-3 gene.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085580; BAB92962.1; -.
DR GO; GO:0030893; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBENZIME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868BDAB9 CRC64;

Query Match      18.4%; Score 401; DB 6; Length 277;
Best Local Similarity 32.2%; Pred. No. 1.3e-27;
Matches 88; Conservative 51; Mismatches 92; Indels 42; Gaps 5;

QY 150 DLAYILMEPCGHCLIIINNVPFCRESGLTRTGSNIDCEKLRFRFSSHLFMVEVKGLTA 209
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
34 DNSYKWDYPEMGLCIINNKNFHKSTGMAPRSGTDVDAANLRETFTNLKYEVRNNDLTC 93
QY 210 KMWLALLELARQDHGALDCCVVWVILSHGCGASHLQFPQAVYGTGCPVSVKIVNIENG 269
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
94 EEILLEMNSVSKEDHSKSSFCVLLSHGDE-----GIIFGTNG-FVDLRKVTGTFRG 145
QY 270 TSCPSLGGKPKLFTIQACGGKQKHGFEVASTPEDESFGSNPEPDATPFQEGLTQDQL 329
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
146 DYCRSLTGKPKLFTIQACRGTELDGCIETDSGIEDDM----- 182
QY 330 DAISSLPTPSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVAN 389
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
183 -ACOKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKLYAHKLEFPHILTRVR 241
QY 390 AV-----SVKGIY---KMPGCFNFKKLF 412
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
242 KVATEFESFLDSAFHGKQIPICIVSMLTRELY 274

```

Search completed: August 3, 2004, 09:02:42
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:55:11 ; Search time 54 Seconds
(without alignments)
2176.662 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 2180

Sequence: 1 MDEADRRLLRRCLRLVSEL.....YKQMGCFNFKLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1373613

Minimum DB seq length: 0
Maximum DB seq length: 416

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2180	100.0	416	2	AAW39209	Human ICE
2	2180	100.0	416	4	AAE00606	Human cas
3	2166	99.4	416	6	ADA10646	Human cas
4	2158	99.0	416	6	ADA10674	Human cas
5	2157	98.9	416	2	AA211723	Amino aci
6	2157	98.9	416	5	ABJ01224	Human cas
7	2153	98.8	416	4	AA667375	Amino aci
8	2153	98.8	416	4	AAU08315	Human asp
9	2153	98.8	416	4	AAE08938	Mammalian
10	2153	98.8	416	4	AA84374	Amino aci
11	2153	98.8	416	6	ABB82738	Human cas
12	2153	98.8	416	8	ADE52020	Human mam
13	2150	98.6	416	6	ADA10675	Human cas
14	2144	98.3	416	6	ADA10676	Human cas
15	2069.5	94.9	401	6	ADA10677	Human cas
16	1288	59.1	266	4	AAE00620	Human cas
17	1083	49.7	203	3	AAW39208	Human ICE
18	468	21.5	93	5	ABJ04760	Caspase-9
19	420	19.3	277	4	AA678712	Pig caspa
20	418	19.2	249	3	AAE26763	Human cas
21	418	19.2	277	2	AAW00372	Apopain C
22	418	19.2	277	2	AAW16600	Apopain C
23	418	19.2	277	2	AAW95831	Human int
24	418	19.2	277	2	AAW00677	Pro-Yama.
25	418	19.2	277	2	AAW41688	Amino aci

26	418	19.2	277	2	AA211717	Amino aci
27	418	19.2	277	4	AAU05394	Human cas
28	418	19.2	277	4	AAU05395	Mouse cas
29	418	19.2	277	4	AA800600	Human cas
30	418	19.2	277	5	ABG30904	Human mem
31	418	19.2	277	5	ABJ01218	Human cas
32	418	19.2	277	6	AAQ19867	Bacteriop
33	418	19.2	277	7	ADD25641	Binding d
34	418	19.2	277	7	AD63082	Human Pro
35	416.5	19.1	245	4	AA859579	Human cas
36	414.5	19.0	261	4	AAE00610	Chimeric
37	414	19.0	241	4	AA898654	Caspase-3
38	409	18.8	277	2	AAW47089	Rat inter
39	409	18.8	277	7	AD63080	Rat Prote
40	408	18.7	277	2	AAW48937	Mutant hu
41	408	18.7	277	2	AAW48937	Mutant hu
42	378	17.3	286	3	AA56997	Human pro
43	378	17.3	286	4	AA859578	Human cas
44	374	17.2	254	4	AA898656	Caspase-8
45	361.5	16.6	244	4	AA898655	Caspase-7

ALIGNMENTS

RESULT 1
AAW39209
ID AAW39209 standard; peptide; 416 AA.
XX
AC AAW39209;
XX
XX
DT 18-MAY-1998 (first entry)
XX
DE Human ICE LAP-6 polypeptide.
XX
XX
KW ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;
KW Viral infection; tumour; inflammation; osteoporosis; AIDS; human;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
FN EP808904-A2.
XX
XX
PD 26-NOV-1997.
XX
PF 19-MAY-1997; 97EP-00303397.
XX
PR 20-MAY-1996; 96US-0017949P.
PR 23-MAY-1996; 96US-0020344P.
PR 05-JUN-1996; 96US-0018961P.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
PA (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
PI Dixit VM, He W, Ruben SM, Kikly KK;
XX
XX WPI; 1998-001790/01.
DR N-PSDB; AAV03401.
XX
XX
XX
PT DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -
PT useful to develop products to treat, e.g. viral infection, tumour,
XX Alzheimer's disease, inflammation, osteoporosis and AIDS.
XX
PS Claim 4; Fig 1; 44pp; English.
XX
CC This is a human interleukin-1 beta converting enzyme apoptosis protease-6
CC (ICE LAP-6) polypeptide. The ICE LAP-6 polypeptide and agonists to the
CC polypeptide can be used to induce apoptosis, e.g. as an antiviral or
CC antitumour agent, control embryonic development and tissue homeostasis
CC and the roles of such factors in dysfunction and disease. Antagonists
CC which inhibit the activity of the ICE LAP-6 polypeptide can be used to
CC treat, Alzheimer's or Parkinson's disease, rheumatoid arthritis, septic

CC shock, sepsis, stroke, chronic, acute or central nervous system
 CC inflammation, osteoporosis, ischaemia reperfusion injury, cell death
 CC associated with cardiovascular disease, polycystic kidney disease,
 CC apoptosis of endothelial cells in cardiovascular disease, degenerative
 CC liver disease, multiple sclerosis, cerebellar degeneration, ischaemic
 CC injury, myocardial infarction, acquired immunodeficiency syndrome (AIDS),
 CC myelodysplastic syndrome, aplastic anaemia, male pattern baldness and
 CC head injury damage. They can also be used for detection and diagnosis
 XX
 SQ Sequence 416 AA;

Query Match 100.0%; Score 2180; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1e-219;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 Db 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPEIRKPEV 120
 Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPEIRKPEV 120
 QY 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180
 Db 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180
 QY 181 TGSNIDCEKLRFRFSSLHFVVEYKGDLTAKKVMALLLELALRQDHGALDCCVVILSHGQ 240
 Db 181 TGSNIDCEKLRFRFSSLHFVVEYKGDLTAKKVMALLLELALRQDHGALDCCVVILSHGQ 240
 QY 241 ASHLQPPGAVYTGDCPVSVKEIWNIPNGTSCPSLGGKPKLFTIQACGGKQDHGFVAS 300
 Db 241 ASHLQPPGAVYTGDCPVSVKEIWNIPNGTSCPSLGGKPKLFTIQACGGKQDHGFVAS 300
 QY 301 TSPEDSPGSPNPPDPTPQEGRLTDFDQDAISLTPSPDIFVSYSTFFGFSVRDPKSG 360
 Db 301 TSPEDSPGSPNPPDPTPQEGRLTDFDQDAISLTPSPDIFVSYSTFFGFSVRDPKSG 360
 QY 361 SMYVETLDDIFEQWAHSEDLSLLRVANAVSVKGIYKQMPGCFNLRKLPKTS 416
 Db 361 SMYVETLDDIFEQWAHSEDLSLLRVANAVSVKGIYKQMPGCFNLRKLPKTS 416

RESULT 2

AAE00606
 ID AAE00606 standard; protein; 416 AA.

AC AAE00606;

XX 02-JUL-2001 (first entry)

DT Human caspase-9, alternative version.

DE Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6;
 XX cysteine protease; apoptosis; caspase expression cassette; metastasis;
 XX tumour; cathepsin B; urokinase; proliferation; gene therapy.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 28 /note= "Encoded by GCC; Ala is present in the sequence
 shown in page 105-107 (AAE00620) "

FT Misc-difference 96 /note= "Encoded by GCA; Ala is present in the sequence
 shown in page 105-107 (AAE00620) "

FT Misc-difference 139..290 /note= "Encoded by GTCGAG; Amino acid residues from
 position 140 to 289 present in this sequence are not
 found in the sequence shown in page 105-107 (AAE00620) "

FT Cleavage-site 315..316 /label= Proteolytic_cleavage_site

FT Cleavage-site 330..331
 FT /label= Proteolytic_cleavage_site

XX WO200129232-A2.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-US028941.

XX 20-OCT-1999; 99US-0160559P.

XX 14-AUG-2000; 2000US-0225564P.

XX (SCIO-) SCIOS INC.

XX Cordell B, Li Y;

XX WPI; 2001-290920/30.

XX N-PSDB; AAD03916.

XX Novel fusion polypeptide comprising first and second caspase subunit
 PT separated by cleavage site not associated in nature with caspase subunit,
 PT useful for cloning gene encoding enzymes involved in proteolytic
 PT cleavage.

XX Claim 4; Fig 18; 116pp; English.

XX The present sequence is an alternative version of human Caspase-9 also
 CC known as interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases
 CC are a family of cysteine proteases, that participate in the initiation
 CC and execution of apoptosis. Caspases exist as pro-enzymes, activated by
 CC cleavage into a large and small subunit, occurring after specific
 CC aspartic acid residues within the pro-enzyme sequence. The present
 CC invention relates to a method for functional cloning of genes encoding
 CC proteins or enzymes involved in proteolytic cleavage. The invention is
 CC based on the use of caspase expression cassettes comprising the coding
 CC sequence of a proteolytic cleavage site flanked by sequences encoding two
 CC caspase subunits. A fusion polypeptide comprising a first and a second
 CC caspase subunit, separated by a cleavage site not associated in nature,
 CC is useful for cloning gene encoding enzymes involved in proteolytic
 CC cleavage. An expression cassette containing fusion polypeptide is used to
 CC identify a mutant cell line deficient in an enzyme of interest and is
 CC also useful for diagnosis and suppression of proliferation or metastases
 CC of a tumour cell characterised by overexpression of a polypeptide (e.g.
 CC Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
 CC encoding fusion polypeptide is used in gene therapy. Note: This sequence
 CC SEQ.ID.NO.18 is stated as being the same as that shown in page 105-107
 CC (See AAE00620) in the specification. However these sequences differ at
 CC several positions
 XX

SQ Sequence 416 AA;

Query Match 100.0%; Score 2180; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1e-219;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

Db 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPEIRKPEV 120

Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPEIRKPEV 120

QY 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180

Db 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSSLHFVVEYKGDLTAKKVMALLLELALRQDHGALDCCVVILSHGQ 240

Db 181 TGSNIDCEKLRFRFSSLHFVVEYKGDLTAKKVMALLLELALRQDHGALDCCVVILSHGQ 240

QY 241 ASHLQPPGAVYTGDCPVSVKEIWNIPNGTSCPSLGGKPKLFTIQACGGKQDHGFVAS 300

XX

Db 241 ASHLQFPGAVYGTGCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
 QY 301 TSPEDSPGNSPEPDATPFQEGRLTFDQDAISSLPTSDIFVSVSTFFGFSWRDPKSG 360
 Db 301 TSPEDSPGNSPEPDATPFQEGRLTFDQDAISSLPTSDIFVSVSTFFGFSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKMPGCFNLRKLFKFTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKMPGCFNLRKLFKFTS 416

RESULT 3

ADA10674
 ID ADA10674 standard; protein; 416 AA.

XX AC ADA10646;

DT 06-NOV-2003 (first entry)

XX Human caspase-9 protein.

XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease.

XX OS Homo sapiens.

XX PN US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

PR 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

PI WPI; 2003-219992/21.

DR N-PSDB; ADA10661.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 FT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

XX Claim 36; Page 25-26; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 PS polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,

CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the full length caspase-9 protein.

XX Sequence 416 AA;

Query Match 99.4%; Score 2166; DB 6; Length 416;

Best Local Similarity 99.3%; Pred. No. 3e-218; 2; Indels 0; Gaps 0;
 Matches 413; Conservative 1; Mismatches 2;

QY 1 MDEADRLRLRCRLRLVELEQVDQLMDVLLSRELFPHMIEDIQAGSGSRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVELEQVDQLMDVLLSRELFPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120

Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120

QY 121 LRPEPRPVVDIGSGGPDVGALESRLGNADLAYILSMFPGHCLIIINNVCRESGLRTR 180

Db 121 LRPEPRPVVDIGSGGPDVGALESRLGNADLAYILSMFPGHCLIIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSSLFHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVILSHGQQ 240

Db 181 TGSNIDCEKLRFRFSSLFHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVILSHGQQ 240

QY 241 ASHLQFPGAVYGTGCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300

Db 241 ASHLQFPGAVYGTGCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300

QY 301 TSPEDSPGNSPEPDATPFQEGRLTFDQDAISSLPTSDIFVSVSTFFGFSWRDPKSG 360

Db 301 TSPEDSPGNSPEPDATPFQEGRLTFDQDAISSLPTSDIFVSVSTFFGFSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKMPGCFNLRKLFKFTS 416

Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKMPGCFNLRKLFKFTS 416

RESULT 4

ADA10674

ID ADA10674 standard; protein; 416 AA.

XX AC ADA10674;

XX 06-NOV-2003 (first entry)

XX Human caspase-9 protein D315A mutant.

XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; mutein.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 315 /note= "Wild-type Asp substituted by Ala"

XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

```

PR 08-FEB-2001; 2001US-0267966P.
PR 24-AUG-2001; 2001US-00939293.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Alnemri ES;
XX WPI; 2003-219992/21.
XX
XX New nucleic acid molecules encoding a peptide or polypeptide that binds
XX to a portion of an inhibitor of apoptosis protein, useful for inducing
XX apoptosis and identifying inhibitors or enhancers of apoptosis for
XX treating AIDS, or cancer.
XX
XX Claim 36; Page; 52pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX (comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically
XX binds at least a portion of an IAP and a second portion of a procaspase-9
XX containing a mutated active site, where the peptide or polypeptide
XX specifically binds at least a portion of an IAP and lacks cysteine
XX protease activity, and at least a portion of caspase-3, where the peptide
XX or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
XX an IAP or an IAP Bir3 domain) or at least a portion of a mutated
XX procaspase-9, which fails to undergo normal processing and possesses wild
XX type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
XX polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
XX expression vector comprising any of the nucleic acids, a host cell
XX containing the expression vector, an antibody that specifically binds to the
XX peptide or polypeptide, an antibody that specifically binds to an
XX epitope located on the N-terminus of a caspase-9-pl2, inducing apoptosis
XX in a cell or stimulating apoptosis in a neoplastic or tumour cell,
XX identifying an inhibitor or enhancer of caspase-mediated apoptosis,
XX identifying a compound that inhibits the peptide or polypeptide,
XX producing a compound for inhibiting or enhancing apoptosis in a cell, and
XX a process for the manufacture of a compound for inhibiting or enhancing
XX apoptosis in a cell. The nucleic acid molecules and peptides or
XX polypeptides are useful for inducing apoptosis and identifying inhibitors
XX or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
XX ischaemic injury, cancer, autoimmune diseases. The present sequence
XX represents the caspase-9 protein mutated to ablate the autocatalytic
XX cleavage site in the linker region. Note: the present sequence is not
XX shown in the specification but was created by the indexer using the
XX information in the claims and the wild type caspase-9 sequence.
XX
XX SQ Sequence 416 AA;
XX
XX Query Match 99.0%; Score 2158; DB 6; Length 416;
XX Best Local Similarity 99.0%; Pred. No. 2.1e-217;
XX Matches 412; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
XX Db 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
XX
XX QY 61 DLTRGSQALPLFTSCLEDTGQDMLASFLTRNQAGKLSKPTLENLTPVVLREIRKPEV 120
XX Db 61 DLTRGSQALPLFTSCLEDTGQDMLASFLTRNQAGKLSKPTLENLTPVVLREIRKPEV 120
XX
XX QY 121 LRPEFRPVDIGSGGFGDVGALSLRGNADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
XX Db 121 LRPEFRPVDIGSGGFGDVGALSLRGNADLAVILSMPCGHCLIIINNVMFCRESGLRTR 180
XX
XX QY 181 TGSNIDCEKLRRFSSHFVVEVKGDLTAKKMWLALLELARQHGALDCCVVILSHGCQ 240
XX Db 181 TGSNIDCEKLRRFSSHFVVEVKGDLTAKKMWLALLELARQHGALDCCVVILSHGCQ 240
XX
XX QY 241 ASHLQFPGAVYTGDCPVSVKEKIVNIENGTSCPSLGKPKLFFIOACGSGKDHGEVAS 300
XX
XX Db 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
XX 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

```

```

Db 241 ASHLQFPGAVYTGDCPVSVKEKIVNIENGTSCPSLGKPKLFFIOACGSGKDHGEVAS 300
QY 301 TSPDESPGSNPEDATPFQGLRFTDQDAISSLPTSDIFVSVYSTPFGFVSWRDPKSG 360
Db 301 TSPDESPGSNPEDATPFQGLRFTDQDAISSLPTSDIFVSVYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCCFNFLRKLFFKTS 416
Db 361 SWYVETLDDIEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCCFNFLRKLFFKTS 416
XX
XX RESULT 5
XX AAY21723
XX ID AAY21723 standard; protein; 416 AA.
XX AC AAY21723;
XX DT 10-SEP-1999 (first entry)
XX DE Amino acid sequence of caspase-9 (ICE-LAP6).
XX KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
XX KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
XX KW tumour cell; myocardial infarction; human.
XX OS Homo sapiens.
XX FN WO9935277-A2.
XX PD 15-JUL-1999.
XX PF 11-JAN-1999; 99WO-US000632.
XX PR 09-JAN-1998; 98US-0070987P.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Alnemri ES;
XX DR WPI; 1999-419353/35.
XX DR N-PSDB; AAX81225.
XX PT New isolated nucleic acid molecule encoding a rev-caspase - used for
XX PT screening and identifying inhibitors or enhancers for treating cancer or
XX PT autoimmune disease.
XX PS Disclosure; Fig 19A-B; 74pp; English.
XX
XX The invention relates to nucleic acid molecules encoding rev-caspases.
XX Rev-caspases are cysteine proteases that specifically cleave proteins
XX after Asp residues and is expressed as a zymogen, in which the small
XX subunit is N-terminal to a large subunit. A gene delivery vehicle
XX comprising a rev-caspase coding sequence is useful for the treatment of
XX cancer, where the gene delivery vehicle is internalised by tumour cells.
XX The gene delivery vehicle can also be used to treat autoimmune diseases.
XX Cells transfected with a rev-caspase expressing vector can be used in
XX identification of inhibitors or enhancers of caspase-mediated apoptosis.
XX In vitro translated rev-caspase can be used to identify an inhibitor or
XX enhancer of caspase processing activity. Caspase inhibitors are useful
XX for treating neurodegenerative diseases as well as for inhibiting
XX apoptosis in the heart following myocardial infarction. Sequences
XX AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
XX gene products (AAY21715-Y21724)
XX
XX SQ Sequence 416 AA;
XX
XX Query Match 98.9%; Score 2157; DB 2; Length 416;
XX Best Local Similarity 99.0%; Pred. No. 2.6e-217;
XX Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
XX Db 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

```

```
QY 61 DLETRGSQALPLFISCLDGTQDMFLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMFLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFGDVGALESURGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
Db 121 LRPETPRVDIGSGGFGDVGALESURGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVWVILSHGQC 240
Db 181 TGSNIDCEKLRSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVWVILSHGQC 240
QY 241 ASHLQFPQAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQFPQAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISSLTPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISSLTPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 6
ID ABJ01224 standard; protein; 416 AA.
XX AC ABJ01224;
DT 18-SEP-2002 (first entry)
DE Human caspase-9 SEQ ID NO: 30.
XX
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
KW autoimmune disease; cytostatic; immunosuppressive.
XX
XX Homo sapiens.
XX
XX US6376226-B1.
XX
XX 23-APR-2002.
XX
XX 26-APR-2000; 2000US-00561756.
XX
XX 09-JAN-1998; 98US-0070897P.
XX 08-JAN-1999; 99US-00227721.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-453146/48.
XX DR N-PSDB; ABT03972.
XX
XX New rev-caspases engineered to contain the small subunit fused in frame N
XX -terminal to the large subunit, which is in reverse order to the wild
XX type caspases, are useful to treat cancer and autoimmune diseases.
XX
XX Disclosure; Fig 19; 81pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
XX can be used in the gene therapy of cancer and autoimmune diseases. The
XX present sequence is a protein described in the exemplification of the
XX invention
XX
XX Sequence 416 AA;
```

Query Match 98.9%; Score 2157; DB 5; Length 416;
Best Local Similarity 99.0%; Pred. No. 2.6e-217;

```
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFPRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFPRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMFLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMFLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFGDVGALESURGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
Db 121 LRPETPRVDIGSGGFGDVGALESURGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVWVILSHGQC 240
Db 181 TGSNIDCEKLRSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVWVILSHGQC 240
QY 241 ASHLQFPQAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQFPQAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISSLTPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISSLTPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 7
AAG67375
ID AAG67375 standard; protein; 416 AA.
XX AC AAG67375;
XX
XX 13-NOV-2001 (first entry)
XX
XX Amino acid sequence of human Mch6 polypeptide.
XX
XX Mch6; ced-3 homologue; ICE; interleukin-1-beta converting enzyme;
XX aspartate-specific cysteine protease; ASCP; apoptotic cell death;
XX Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX retinitis pigmentosa; cerebellar degeneration; myelodysplastic syndrome;
XX aplastic anemia; ischemic injury; myocardial infarction; stroke; cancer;
XX reperfusion injury; autoimmune disease; systemic lupus erythematosus;
XX immune-mediated glomerulonephritis; viral infection; cell death.
XX
XX Homo sapiens.
XX
XX US6274318-B1.
XX
XX 14-AUG-2001.
XX
XX 13-MAY-1999; 99US-00311760.
XX
XX 29-MAY-1997; 97US-00865579.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX WPI; 2001-540372/60.
XX DR N-PSDB; AAH77927.
XX
XX Identifying mammalian homolog ced-3 homolog (Mch)6 activity modulators,
XX useful for treating lymphomas, carcinomas and hormone dependent tumors,
XX Alzheimer's disease, Parkinson's disease, comprises using Mch6
XX polypeptide.
XX
XX Example 1; Fig 1a-c; 36pp; English.
XX
```

CC The present sequence represents a human Mch6 polypeptide. Mch6 is a ced-3
 CC homologue, and is a member of the ICE (interleukin-1-beta converting
 CC enzyme) family of aspartate-specific cysteine proteases (ASCPs). The
 CC specification describes a method for identifying mammalian Mch6 activity
 CC modulators (inhibitors or enhancers). The compounds identified by the
 CC method are useful as pharmaceuticals for treating or preventing diseases
 CC characterized by increased apoptotic cell death such as Alzheimer's
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, or cerebellar degeneration, myelodysplastic syndromes such as
 CC aplastic anemia, ischemic injury including myocardial infarction, stroke
 CC and reperfusion injury. The compounds are also useful for treating
 CC diseases characterized by loss of apoptotic cell death such as cancers,
 CC e.g. lymphomas, carcinomas and hormone dependent tumours such as breast,
 CC prostate and ovarian cancer. Increased cell survival or apoptosis
 CC inhibition also results in autoimmune diseases such as systemic lupus
 CC erythematosus and immune-mediated glomerulonephritis as well as viral
 CC infections such as herpes virus, pox virus and adenovirus and the novel
 CC identified compounds are useful for treating these conditions. The Mch6
 CC inhibitors are used to treat or to reduce severity of diseases
 CC characterized by increased programmed cell death
 XX
 SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;

Best Local Similarity 98.8%; Pred. No. 6.9e-217;

Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVLDLWVLLSLRFLRPHMIEDIQAGSGRRDQARQLII 60
 Db 1 MDEADRLRLRCRLRLVEELQVLDLWVLLSLRFLRPHMIEDIQAGSGRRDQARQLII 60
 QY 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAQKLSKPTLENTTPVVLPEIRKPEV 120
 Db 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAQKLSKPTLENTTPVVLPEIRKPEV 120
 QY 121 LRPEPRPVDIGGGFGDVGALSLRGNADLAYILSMPCGCHLIINNVCRESGLRTR 180
 Db 121 LRPEPRPVDIGGGFGDVGALSLRGNADLAYILSMPCGCHLIINNVCRESGLRTR 180
 QY 181 TGSNIDCEKLRRLRRFSSILHFVVEYKGDLTAKKMWLALLELARODHGALDCVWVILSHGQ 240
 Db 181 TGSNIDCEKLRRLRRFSSILHFVVEYKGDLTAKKMWLALLELARODHGALDCVWVILSHGQ 240
 QY 241 ASHLQFPAGVYGTGCPVSVKEKIVNFNGTSCPSLGKPKLFITQACGQKDHGEVAS 300
 Db 241 ASHLQFPAGVYGTGCPVSVKEKIVNFNGTSCPSLGKPKLFITQACGQKDHGEVAS 300
 QY 301 TSPEDSPGSNPEDPATPFQEGRLTFDQDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
 Db 301 TSPEDSPGSNPEDPATPFQEGRLTFDQDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPCCGFNLRKLPFKTS 416
 Db 361 SWYVETLDDIFFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPCCGFNLRKLPFKTS 416

RESULT 8

AAU08315

ID AAU08315 standard; protein; 416 AA.

XX AAU08315;

AC AAU08315;

DT 04-DEC-2001 (first entry)

DE Human aspartate-specific cysteine protease, MCH6.

XX Human; aspartate-specific cysteine protease; MCH6; neutropic;

KW neuroprotective; anti-Parkinsonian; antianemic; vasotropic; cardiant;

KW cerebroprotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;

KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;

KW cerebellar degeneration; myelodysplastic syndrome; aplastic anaemia;

KW ischaemic injury; myocardial infarction; stroke; reperfusion injury;

KW amyotrophic lateral sclerosis.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Active-site 285..289
 FT Cleavage-site 312..316
 FT /label= Granzyme_beta_cleavage_site
 FT /note= "Cleavage occurs after Asp at position 315"
 FT Cleavage-site 327..331
 FT /label= Granzyme_beta_cleavage_site
 FT /note= "Cleavage occurs after Asp at position 330"
 XX
 US2001016345-A1.
 XX 23-AUG-2001.
 XX 22-DEC-2000; 2000US-00746731.
 XX 29-MAY-1997; 97US-008665579.
 PR 25-FEB-1999; 99US-00257218.
 XX
 XX (ALNE/) ALNEMRI E S.
 PA (FERN/) FERNANDES-ALNEMRI T.
 PA (LITW/) LITWACK G.
 XX
 PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX
 DR WPI; 2001-535542/59.
 DR N-PSDB; AAS12629.
 XX
 PT New Mch6 polypeptides and genes encoding the polypeptides useful for
 PT diagnosing, treating or reducing the severity of cell death-mediated
 PT diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
 PT Parkinson's disease.
 XX
 PS Claim 8; Fig 1; 15pp; English.
 XX
 CC The invention relates to an isolated gene encoding MCH6 (mammalian ced-3
 CC homologue 6) an aspartate-specific cysteine protease and the MCH6
 CC polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
 CC to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
 CC death-mediated diseases (i.e. apoptotic) such as neurodegenerative
 CC diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
 CC myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
 CC myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
 CC nucleic acids and polypeptides can also be used to diagnose or generate
 CC reagents to diagnose diseases mediated or characterised by programmed
 CC cell death. A purified recombinant MCH6 protein can be used to measure
 CC hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
 CC a continuous fluorometric assay. The present sequence represents human
 CC MCH6
 XX
 SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;

Best Local Similarity 98.8%; Pred. No. 6.9e-217;

Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVLDLWVLLSLRFLRPHMIEDIQAGSGRRDQARQLII 60
 Db 1 MDEADRLRLRCRLRLVEELQVLDLWVLLSLRFLRPHMIEDIQAGSGRRDQARQLII 60
 QY 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAQKLSKPTLENTTPVVLPEIRKPEV 120
 Db 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAQKLSKPTLENTTPVVLPEIRKPEV 120
 QY 121 LRPEPRPVDIGGGFGDVGALSLRGNADLAYILSMPCGCHLIINNVCRESGLRTR 180
 Db 121 LRPEPRPVDIGGGFGDVGALSLRGNADLAYILSMPCGCHLIINNVCRESGLRTR 180
 QY 181 TGSNIDCEKLRRLRRFSSILHFVVEYKGDLTAKKMWLALLELARODHGALDCVWVILSHGQ 240
 Db 181 TGSNIDCEKLRRLRRFSSILHFVVEYKGDLTAKKMWLALLELARODHGALDCVWVILSHGQ 240

Db 181 TGSNIDCEKLRRRSSPHFMVEVKGDLTAKKMWLALLELAQQDHGALDCCVVVILSHGQC 240

QY 241 ASHLQFPGAVYGTDCGCVSVKEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

Db 241 ASHLQFPGAVYGTDCGCVSVKEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

QY 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360

Db 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 9

AAE08938

ID AAE08938 standard; protein; 416 AA.

XX

AC AAE08938;

DT 15-NOV-2001 (first entry)

XX

DE Mammalian ced-3 homologue 6 (Mch6).

XX

KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;

KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;

KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;

KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;

KW viral infection; cell death-mediated disease; neuroprotective.

XX

OS Unidentified.

XX

FH Key

FT Active-site 285..290

FT Cleavage-site 315..316

FT Cleavage-site 330..331

XX

PN US6271361-B1.

XX

PD 07-AUG-2001.

XX

PF 25-FEB-1999; 99US-00257218.

XX

PR 29-MAY-1997; 97US-00865579.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX

PI Alnemri ES, Fernandes-Alnemri T, Litwack G;

DR WPI; 2001-528686/58.

DR N-PSDB; AAD15656.

XX

PT New apoptotic genes and their apoptotic protease products, useful for

PT modulating apoptosis for the therapeutic treatment of human diseases,

PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's

PT disease.

XX

PS Claim 2; Fig 1; 36pp; English.

XX

CC The invention relates to an isolated gene encoding apoptic protease,

CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-

CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences

CC are useful for modulating apoptosis for the therapeutic treatment of

CC human diseases. Mch6 sequences are useful for upregulating apoptosis

CC (e.g. for treating cancers, autoimmune disease or viral infections) or

CC downregulating apoptosis (e.g. for treating Alzheimer's disease,

CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is

CC useful for diagnosing, treating or reducing the severity of cell death-

CC mediated diseases, as well as other diseases mediated by either increased

CC or decreased programmed cell death. The present amino acid sequence is

CC Mch6

XX SQ Sequence 416 AA;

Query Match

Best Local Similarity 98.8%; Score 2153; DB 4; Length 416;

Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSSELFRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFTISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLPEIRKPEV 120

Db 61 DLETRGSQALPLFTISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLPEIRKPEV 120

QY 121 LRPTPRVDIGSGGFGDVGALESRLGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180

Db 121 LRPTPRVDIGSGGFGDVGALESRLGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRRRSSPHFMVEVKGDLTAKKMWLALLELAQQDHGALDCCVVVILSHGQC 240

Db 181 TGSNIDCEKLRRRSSPHFMVEVKGDLTAKKMWLALLELAQQDHGALDCCVVVILSHGQC 240

QY 241 ASHLQFPGAVYGTDCGCVSVKEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

Db 241 ASHLQFPGAVYGTDCGCVSVKEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

QY 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360

Db 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 10

AAE08938

ID AAE08938 standard; protein; 416 AA.

XX

AC AAE08938;

XX

DT 22-AUG-2001 (first entry)

XX

DE Amino acid sequence of aspartate-specific cysteine protease Mch6.

XX

KW Human; apoptotic protease; Mch6; aspartate-specific cysteine protease;

KW cell death; cancer; autoimmune disease; systemic lupus erythematosus;

KW viral infection; degenerative disorder; Alzheimer's disease;

KW Parkinson's disease; myelodysplastic syndrome; myocardial infarction;

KW stroke.

XX

OS Homo sapiens.

XX

PN US2001006779-Al.

XX

PD 05-JUL-2001.

XX

PF 29-MAY-1997; 97US-00865579.

XX

PR 29-MAY-1997; 97US-00865579.

XX

PA (ALNE/) ALNEMRI E S.

PA (FERN/) FERNANDES-ALNEMRI T.

PA (LITW/) LITWACK G.

XX

PI Alnemri ES, Fernandes-Alnemri T, Litwack G;

DR WPI; 2001-389294/41.

DR N-PSDB; AAE08938.

XX

PT Isolated gene encoding a human apoptotic protease known as Mch6, useful

PT in the diagnosis or treatment of cell death-mediated conditions, e.g.

PT cancers and autoimmune diseases such as systemic lupus erythematosus.

XX Claim 8; Fig 1A-C; 15pp; English.

XX The present sequence represents a human apoptotic protease, designated
 CC Mch6. Mch6 is an aspartate-specific cysteine protease. Mch6 polypeptides
 CC and polynucleotides can be used to diagnose, treat or reduce the severity
 CC of cell death-mediated conditions, e.g. cancers, autoimmune diseases such
 CC as systemic lupus erythematosus, viral infections such as herpesvirus,
 CC degenerative disorders such as Alzheimer's disease and Parkinson's
 CC disease, myelodysplastic syndromes such as myocardial infarction and
 CC stroke. They can also be used to screen for compounds that inhibit or
 CC promote Mch6 mediated apoptosis

XX Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
 Best Local Similarity 98.8%; Pred. No. 6.9e-217;
 Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQRAGSSRRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQRAGSSRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120

Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180

Db 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRFSLSHFVVEKGLDTAKKMWLALLELARDHGLDCCVVVILSHGCG 240

Db 181 TGSNIDCEKLRRLRFSLSHFVVEKGLDTAKKMWLALLELARDHGLDCCVVVILSHGCG 240

QY 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300

Db 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300

QY 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360

Db 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

RESULT 11

ABB82738

ID ABB82738 standard; protein; 416 AA.

XX AC ABB82738;

XX 07-MAR-2003 (first entry)

XX Human caspase-9 polypeptide.

XX Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human.

XX Homo sapiens.

XX WO200290931-A2.

XX 14-NOV-2002.

XX 07-MAY-2002; 2002WO-US014487.

XX 07-MAY-2001; 2001US-0289223P.

XX 12-FEB-2002; 2002US-0356934P.

XX (BURN-) BURNHAM INST.

XX

PT Reed JC;

XX WPI; 2003-111999/10.

XX Determining a prognosis for survival for a cancer patient, useful for
 PT determining if the patient is at risk for relapse, comprises measuring a
 PT level of TUCAN in a sample from the patient, and comparing it to a
 PT reference level.

XX Example; Page 125-126; 153pp; English.

XX The invention relates to determining a prognosis for survival for a
 CC cancer patient. The method involves (a) measuring a level of a tumour up-
 CC regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
 CC cell-containing sample from the cancer patient; and (b) comparing the
 CC level of TUCAN in the sample to a reference level of TUCAN, where a low
 CC level of TUCAN in the sample correlates with increased survival of the
 CC patient. Alternatively, the method involves measuring levels of TUCAN and
 CC one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
 CC Smac in a neoplastic cell-containing sample from the cancer patient. The
 CC method is useful for determining if the patient is at risk for relapse,
 CC or for determining a proper course of treatment for a patient with
 CC cancer. The method is also useful for monitoring the effectiveness of a
 CC course of treatment for a patient with cancer, e.g. colon cancer,
 CC gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
 CC leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
 CC present sequence represents a human caspase-9 polypeptide

XX Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 6; Length 416;

Best Local Similarity 98.8%; Pred. No. 6.9e-217;

Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQRAGSSRRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQRAGSSRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120

Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180

Db 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRFSLSHFVVEKGLDTAKKMWLALLELARDHGLDCCVVVILSHGCG 240

Db 181 TGSNIDCEKLRRLRFSLSHFVVEKGLDTAKKMWLALLELARDHGLDCCVVVILSHGCG 240

QY 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300

Db 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300

QY 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360

Db 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

RESULT 12

ADE52020

ID ADE52020 standard; protein; 416 AA.

XX AC ADE52020;

XX 29-JAN-2004 (first entry)

XX Human mammalian ced-3 homologue 6 (Mch6).

CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.
XX
XX
SQ Sequence 416 AA;

Query Match 98.6%; Score 2150; DB 6; Length 416;
Best Local Similarity 98.6%; Pred. No. 1.4e-216;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPETRPVDDIGSGGFDGVALESRLGNADLAYILSMPECGHCLINNNVFCRESGLRTR 180
DB 121 LRPETRPVDDIGSGGFDGVALESRLGNADLAYILSMPECGHCLINNNVFCRESGLRTR 180
QY 181 TGSNDCEKLRFRFSSLHFMVVKGLTAKKVVALLLELAROHDGALDCVVVILSHGQQ 240
DB 181 TGSNDCEKLRFRFSSLHFMVVKGLTAKKVVALLLELAROHDGALDCVVVILSHGQQ 240
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DB 241 ASHLQFPAGVYGTDCGVPVSEKIVNFNGTSCPSLGGKPKLFFIOACGGEQKHGFVEVAS 300
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DB 301 TSPDESPGSPNEPATPQEGRLTFDQDAISSLTPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWVETLDDIFQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 361 SWVETLDDIFQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 14
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ID ADA10676 standard; protein; 416 AA.
XX
AC ADA10676;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human caspase-9 protein E306A/D315A/D330A mutant.
XX
KW Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
KW ischaemic injury; cancer; autoimmune disease; mutant; mutein.
XX
OS Synthetic.
OS Homo sapiens.
FH
FH Key Location/Qualifiers
XX
FT Misc-difference 306
FT FT
FT Misc-difference 315

FT
FT Misc-difference 330 /note= "Wild-type Asp substituted by Ala"
FT
XX /note= "Wild-type Asp substituted by Ala"
PN US2002160975-A1.
PD 31-OCT-2002.
XX
PF 06-FEB-2002; 2002US-00068569.
XX
PR 08-FEB-2001; 2001US-0267966P.
PR 24-AUG-2001; 2001US-00939293.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2003-219992/21.
XX
PT New nucleic acid molecules encoding a peptide or polypeptide that binds
PT to a portion of an inhibitor of apoptosis protein, useful for inducing
PT apoptosis and identifying inhibitors or enhancers of apoptosis for
PT treating AIDS, or cancer.
XX
PS Claim 38; Page; 52pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX (comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically
XX binds at least a portion of an IAP and a second portion of a procaspase-9
XX containing a mutated active site, where the peptide or polypeptide
XX specifically binds at least a portion of an IAP and lacks cysteine
XX protease activity, and at least a portion of caspase-3, where the peptide
XX or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
XX an IAP or an IAP Bir3 domain) or at least a portion of a mutated
XX procaspase-9, which fails to undergo normal processing and possesses wild
XX type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
XX polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
XX expression vector comprising any of the nucleic acids, a host cell
XX containing the expression vector, an antibody that specifically binds to
XX the peptide or polypeptide, an antibody that specifically binds to an
XX epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
XX in a cell or stimulating apoptosis in a neoplastic or tumour cell,
XX identifying an inhibitor or enhancer of caspase-mediated apoptosis,
XX identifying a compound that inhibits the peptide or polypeptide,
XX producing a compound for inhibiting or enhancing apoptosis in a cell, and
XX a process for the manufacture of a compound for inhibiting or enhancing
XX apoptosis in a cell. The nucleic acid molecules and peptides or
XX polypeptides are useful for inducing apoptosis and identifying inhibitors
XX or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
XX ischaemic injury, cancer, autoimmune diseases. The present sequence
XX represents the caspase-9 protein mutated to ablate the autocatalytic
XX cleavage site in the linker region. Note: the present sequence is not
XX shown in the specification but was created by the indexer using the
XX information in the claims and the wild type caspase-9 sequence.
XX
SQ Sequence 416 AA;

Query Match 98.3%; Score 2144; DB 6; Length 416;
Best Local Similarity 98.6%; Pred. No. 6.1e-216;
Matches 410; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120

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QY 121 LRPTPRPVDIGSGGFGDVGALSLRGVADLALAYILSMPCGCHLIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGGFGDVGALSLRGVADLALAYILSMPCGCHLIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKKMWLALLELARDHGDALCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKKMWLALLELARDHGDALCCVVVILSHGCQ 240
QY 241 ASHLQFFGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFVEAS 300
Db 241 ASHLQFFGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFVEAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTSDIFVSVSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTSDIFVSVSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPCCFNLKRLKFLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPCCFNLKRLKFLFFKTS 416

RESULT 15
ADAL0677
ID ADAL0677 standard; protein; 401 AA.
AC ADAL0677;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human caspase-9 protein del316-330 mutant.
XX
XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
XX cystostatic; immunosuppressive; inhibitor of apoptosis protein; IAP;
XX caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
XX Bcl3 domain; apoptosis; AIDS; neurodegenerative disease;
XX ischaemic injury; cancer; autoimmune disease; mutant; mutuin.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 315..316
XX /note= "Residues 316-330 of the wild-type protein have
XX been deleted"
XX
XX US2002160975-A1.
XX
XX 31-OCT-2002.
XX
XX 06-FEB-2002; 2002US-00068569.
XX
XX 08-FEB-2001; 2001US-0267966P.
XX 24-AUG-2001; 2001US-00939293.
XX
XX (UWJE-) UNIV JERPERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2003-219992/21.
XX
XX New nucleic acid molecules encoding a peptide or polypeptide that binds
XX to a portion of an inhibitor of apoptosis protein, useful for inducing
XX apoptosis and identifying inhibitors or enhancers of apoptosis for
XX treating AIDS, or cancer.
XX
XX Claim 39; Page; 52pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX (comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically

```

```

CC binds at least a portion of an IAP and a second portion of a procaspase-9
CC containing a mutated active site, where the peptide or polypeptide
CC specifically binds at least a portion of an IAP and lacks cysteine
CC protease activity, and at least a portion of caspase-3, where the peptide
CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
CC an IAP or an IAP Bcl3 domain) or at least a portion of a mutated
CC procaspase-9, which fails to undergo normal processing and possesses wild
CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
CC expression vector comprising any of the nucleic acids, a host cell
CC containing the expression vector, an antibody that specifically binds to
CC the peptide or polypeptide, an antibody that specifically binds to an
CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.
XX
XX Sequence 401 AA;

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Query March 94.9%; Score 2069.5; DB 6; Length 401;
Best Local Similarity 95.7%; Pred. No. 3.9e-208;
Matches 398; Conservative 1; Mismatches 2; Indels 15; Gaps 1;

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Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLDGTQDDMLASFLRTRNQAGKLSKPTLENLTPVWLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDDMLASFLRTRNQAGKLSKPTLENLTPVWLRPEIRKPEV 120

QY 121 LRPTPRPVDIGSGGFGDVGALSLRGVADLALAYILSMPCGCHLIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGGFGDVGALSLRGVADLALAYILSMPCGCHLIINNVPFCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKKMWLALLELARDHGDALCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRFSSLHFVVEVKGDLTAKKMWLALLELARDHGDALCCVVVILSHGCQ 240

QY 241 ASHLQFFGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFVEAS 300
Db 241 ASHLQFFGAVYGTDCGCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFVEAS 300

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTSDIFVSVSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTSDIFVSVSTPFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPCCFNLKRLKFLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPCCFNLKRLKFLFFKTS 401

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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:02:47 ; Search time 45 Seconds
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2166	99.4	416	13 US-10-068-569-1	Sequence 1, Appl
2	2157	98.9	416	9 US-09-954-697-30	Sequence 30, Appl
3	2153	98.8	416	10 US-09-851-873-102	Sequence 102, Appl
4	2153	98.8	416	12 US-09-746-731-2	Sequence 2, Appl
5	2153	98.8	416	13 US-10-059-749-2	Sequence 2, Appl
6	2153	98.8	416	14 US-10-141-618-4	Sequence 4, Appl
7	1282	58.8	266	15 US-10-116-275-172	Sequence 172, App
8	773	35.5	159	12 US-10-424-599-174531	Sequence 174531,
9	468	21.5	93	13 US-10-014-269-27	Sequence 27, Appl
10	468	21.5	93	13 US-10-002-974-27	Sequence 27, Appl
11	468	21.5	93	14 US-10-314-506-27	Sequence 27, Appl
12	419	19.2	277	15 US-10-155-567-4	Sequence 4, Appl
13	418	19.2	264	13 US-10-103-448-3	Sequence 3, Appl
14	418	19.2	264	13 US-10-108-929-3	Sequence 3, Appl
15	418	19.2	277	9 US-09-895-263-4	Sequence 4, Appl

16	418	19.2	277	9 US-09-954-697-12	Sequence 12, Appl
17	418	19.2	277	10 US-09-851-873-98	Sequence 98, Appl
18	418	19.2	277	12 US-10-232-884-4	Sequence 4, Appl
19	418	19.2	277	14 US-10-214-932-108	Sequence 108, App
20	418	19.2	277	14 US-10-207-655-202	Sequence 202, App
21	418	19.2	277	14 US-10-280-670-5	Sequence 5, Appl
22	418	19.2	277	15 US-10-368-438-30	Sequence 30, Appl
23	418	19.2	277	16 US-10-408-765A-172	Sequence 172, App
24	418	19.2	277	16 US-10-701-490-11	Sequence 11, Appl
25	409.5	18.8	284	12 US-10-232-884-5	Sequence 5, Appl
26	378	17.3	286	9 US-09-862-915-1	Sequence 1, Appl
27	371.5	17.0	335	15 US-10-368-438-16	Sequence 16, Appl
28	361.5	16.6	303	9 US-09-944-851-2	Sequence 2, Appl
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37	311.5	14.3	354	9 US-09-888-243-20	Sequence 20, Appl
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39	303.5	13.9	266	15 US-10-368-438-20	Sequence 20, Appl
40	303.5	13.9	293	10 US-09-851-873-99	Sequence 99, Appl
41	303.5	13.9	293	14 US-10-171-077-5	Sequence 5, Appl
42	303.5	13.9	293	14 US-10-280-670-6	Sequence 6, Appl
43	303.5	13.9	293	15 US-10-368-438-31	Sequence 31, Appl
44	294	13.5	147	14 US-10-214-932-110	Sequence 110, App
45	294	13.5	285	9 US-09-954-637-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-10-068-569-1
; Sequence 1, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-1

Query Match	99.4%	Score 2166;	DB 13;	Length 416;
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Db	1	MDEADRLRLRCRLRLVEELQVDQDLWDVLLSRELFRRPHMIEDIQAGSGSRDQARQLII	60	
Qy	61	DLETRGSAFLPFLISCELDTCQDMLASFLRNROAGKLSKPTLENLTVPVLRPEIRKPEV	120	
Db	61	DLETRGSAFLPFLISCELDTCQDMLASFLRNROAGKLSKPTLENLTVPVLRPEIRKPEV	120	
Qy	121	LRPETRPVDIGSGFGDVGGALESIRGNADLAYILSMPCGCHLIINNVCRESGLRTR	180	
Db	121	LRPETRPVDIGSGFGDVGGALESIRGNADLAYILSMPCGCHLIINNVCRESGLRTR	180	
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QY 241 ASHLQPPGAVYGTGDCPVSVKIVNFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTGDCPVSVKIVNFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESPOGSPNPEPATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
Db 301 TSPDESPOGSPNPEPATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
QY 361 SWVETLDDIFQWHAHSEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416
Db 361 SWVETLDDIFQWHAHSEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416
```

```
RESULT 2
US-09-954-697-30
; Sequence 30, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30
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Query Match 98.9%; Score 2157; DB 9; Length 416;
Best Local Similarity 99.0%; Pred. No. 9.1e-206;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVBELOVDQWDLVLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVBELOVDQWDLVLSRELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRQAGKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNDCEKLRRLRRFSLHFMVEVKGDLTAKQWVLALELAQDHGALDCVVVILSHGQ 240
Db 181 TGSNDCEKLRRLRRFSLHFMVEVKGDLTAKQWVLALELAQDHGALDCVVVILSHGQ 240
QY 241 ASHLQPPGAVYGTGDCPVSVKIVNFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTGDCPVSVKIVNFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESPOGSPNPEPATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
Db 301 TSPDESPOGSPNPEPATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
QY 361 SWVETLDDIFQWHAHSEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416
Db 361 SWVETLDDIFQWHAHSEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416
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RESULT 3
US-09-851-873-102
; Sequence 102, Application US/09851873
; Publication No. US2003016548A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kletzien, Rolf P
; APPLICANT: Readon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 102
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-102
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Query Match 98.8%; Score 2153; DB 10; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVBELOVDQWDLVLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVBELOVDQWDLVLSRELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRQAGKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNDCEKLRRLRRFSLHFMVEVKGDLTAKQWVLALELAQDHGALDCVVVILSHGQ 240
Db 181 TGSNDCEKLRRLRRFSLHFMVEVKGDLTAKQWVLALELAQDHGALDCVVVILSHGQ 240
QY 241 ASHLQPPGAVYGTGDCPVSVKIVNFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTGDCPVSVKIVNFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESPOGSPNPEPATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
Db 301 TSPDESPOGSPNPEPATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
QY 361 SWVETLDDIFQWHAHSEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416
Db 361 SWVETLDDIFQWHAHSEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416
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```
RESULT 4
US-09-746-731-2
; Sequence 2, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
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; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-746-731-2

Query Match          98.8%; Score 2153; DB 12; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTPVVLIRPEIRPEV 120
Db 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTPVVLIRPEIRPEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Qy 241 ASHLQFPQAVYGTGCPVSVKEIIVNFGTSCPSLGGKPKLFFIOACGGEOKDHGFEVAS 300
Db 241 ASHLQFPQAVYGTGCPVSVKEIIVNFGTSCPSLGGKPKLFFIOACGGEOKDHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSITFPFGVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSITFPFGVSWRDPKSG 360
Qy 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416
Db 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416

RESULT 5
US-10-059-749-2
; Sequence 2, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
;               Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match          98.8%; Score 2153; DB 13; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTPVVLIRPEIRPEV 120
Db 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTPVVLIRPEIRPEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Qy 241 ASHLQFPQAVYGTGCPVSVKEIIVNFGTSCPSLGGKPKLFFIOACGGEOKDHGFEVAS 300
Db 241 ASHLQFPQAVYGTGCPVSVKEIIVNFGTSCPSLGGKPKLFFIOACGGEOKDHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSITFPFGVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSITFPFGVSWRDPKSG 360
Qy 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416
Db 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416

RESULT 6
US-10-141-618-4
; Sequence 4, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; TITLE OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07

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; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-618-4

Query Match      98.8%; Score 2153; DB 14; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDALSLSELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDALSLSELFRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180

QY 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRFFSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNIDCEKLRRLRFFSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240

QY 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

QY 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 7
US-10-116-275-172
; Sequence 172, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-172

Query Match      58.8%; Score 1282; DB 15; Length 266;
Best Local Similarity 63.2%; Pred. No. 7.1e-119;
Matches 263; Conservative 0; Mismatches 3; Indels 150; Gaps 1;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDALSLSELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDALSLSELFRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180

QY 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRFFSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNIDCEKLRRLRFFSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240

QY 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

QY 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTDCPVSVKEIVNFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWDRPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 8
US-10-424-599-174531
; Sequence 174531, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174531
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12861C.1.pep
US-10-424-599-174531

Query Match      35.5%; Score 773; DB 12; Length 159;
Best Local Similarity 96.9%; Pred. No. 1.7e-68;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTRNQAGLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPE 159
Db 121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPE 159

RESULT 9
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
```



```
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT APPLICATION NUMBER: US/10/014,269
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27
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Query Match          21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
   |||||
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
   |||||

QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
   |||||
Db 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
   |||||
```

```
RESULT 10
US-10-002-974-27
; Sequence 27, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan I.
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-974-27
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```
Query Match          21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
   |||||
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
   |||||

QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
   |||||
Db 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
   |||||
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```
RESULT 11
US-10-314-506-27
; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
```

```
; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,269
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,289
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-506-27
```

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Query Match          21.5%; Score 468; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
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QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
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Db 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
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RESULT 12
US-10-155-567-4
; Sequence 4, Application US/10155567
; Publication No. US20030219421A1
; GENERAL INFORMATION:
; APPLICANT: CHRISTAKOS, Sylvia
; TITLE OF INVENTION: CALBINDIN-D 28K PROTECTION AGAINST GLUCOCORTICOID INDUCED CELL DE
; FILE REFERENCE: 267/266
; CURRENT APPLICATION NUMBER: US/10/155,567
; CURRENT FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 277
; TYPE: PRT
; ORGANISM: homosapiens
US-10-155-567-4
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Query Match          19.2%; Score 419; DB 15; Length 277;
Best Local Similarity 33.2%; Pred. No. 7.4e-33;
Matches 91; Conservative 50; Mismatches 91; Indels 42; Gaps 4;

QY 150 DLAYILSMFPCGHCLIIINNVNFCRESGLRTRTSGNIDCEKLRFFSLHFVVEYKGLTA 209
   |||||
Db 34 DTGKMDYPEWGLCIIINNNKFNHKSIGTSGTDVDAANLRETRNLKYEVRNKNDLTR 93
   |||||

QY 210 KXVLLALELARQDHGALDCCVVVILSHGQASHLOFPFGAVYGTGCPVSVEKIVNIFNG 269
   |||||
Db 94 EEIVELMRDVSKEHDSKRSSFVVCVLLSHGEE-----GIIFGTNG-PVDLKKITNFRG 145
   |||||

QY 270 TSPESLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSPNPDPATPFQEGRLTFDQL 329
   |||||
Db 146 DRCRLTGKPKLFFIQACRGTELDGCIETDGSVDDDM----- 182
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QY 330 DAISSLPTSPDIFVSYSTPFGVSWRDPKSGSVVETLDDIFQWAHSEDLQSLLLRYAN 389
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Db 183 -ACHKIPVDADFLYAYSTAPGYTSWRNSKDGSWFIOSLCAMLKQYADKLEFMHILTRVNR 241
   |||||

QY 390 AVSVK-----GIYKQMPGCFNPLRKKLFF 413
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Db 242 KVATEFESFSFDATFHAKKQIPCIIVSNLTKELYP 275
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RESULT 13

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US-10-103-448-3
; Sequence 3, Application US/10103448
; Publication No. US20020155579A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Wu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D1
; CURRENT APPLICATION NUMBER: US/10/103,448
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-103-448-3

Query Match 19.2%; Score 418; DB 13; Length 264;
Best Local Similarity 33.2%; Pred. No. 8.6e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPECGHCLIIINNVCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGLTA 209
DB 21 DNSYKMDYPEMGLCIIINNKNFKHSTGMTSRSGTDVDAANLRETFRNLYKYEVRNKNDLTR 80

QY 210 KKMVLALLELARQDHGALDCCVVWILSHGCOASHLQFPQAVYGTGDCPVSVEKIVNIENG 269
DB 81 EEIVELMRDVSKEHSHKRSFVCLLSHGEE-----GIIFGTNG-PVDLKKIINFREG 132

QY 270 TSCPSLGGKPKLFFIQACGGQKDHGFVASTSPEDSPGSPNPEPDATPFQEGLRFTDOL 329
DB 133 DCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 169

QY 330 DAISLPTSDIFVSYSTPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVAN 389
DB 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMEHLITVRN 228

QY 390 AVSVK-----GIYKQMPGCFNFKKLPFF 413
DB 229 KVATEFESFSDATPHAKKQIPCIIVSMLTKELYF 262

RESULT 14
US-10-108-929-3
; Sequence 3, Application US/10108929
; Publication No. US20020197702A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Wu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D2
; CURRENT APPLICATION NUMBER: US/10/108,929
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-108-929-3

Query Match 19.2%; Score 418; DB 13; Length 264;
Best Local Similarity 33.2%; Pred. No. 8.6e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPECGHCLIIINNVCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGLTA 209
DB 21 DNSYKMDYPEMGLCIIINNKNFKHSTGMTSRSGTDVDAANLRETFRNLYKYEVRNKNDLTR 80

QY 210 KKMVLALLELARQDHGALDCCVVWILSHGCOASHLQFPQAVYGTGDCPVSVEKIVNIENG 269
DB 81 EEIVELMRDVSKEHSHKRSFVCLLSHGEE-----GIIFGTNG-PVDLKKIINFREG 132

QY 270 TSCPSLGGKPKLFFIQACGGQKDHGFVASTSPEDSPGSPNPEPDATPFQEGLRFTDOL 329
DB 133 DCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 169

QY 330 DAISLPTSDIFVSYSTPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVAN 389
DB 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMEHLITVRN 228

QY 390 AVSVK-----GIYKQMPGCFNFKKLPFF 413
DB 229 KVATEFESFSDATPHAKKQIPCIIVSMLTKELYF 262

RESULT 15
US-09-895-263-4
; Sequence 4, Application US/09895263
; Patent No. US20020076793A1
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; LIKE APOPTOSIS PROTEASE 3 AND 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,263
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-251-6015
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-895-263-4

Query Match 19.2%; Score 418; DB 9; Length 277;
Best Local Similarity 33.2%; Pred. No. 9.3e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPECGHCLIIINNVCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGLTA 209
DB 34 DNSYKMDYPEMGLCIIINNKNFKHSTGMTSRSGTDVDAANLRETFRNLYKYEVRNKNDLTR 93
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Qy	210	KKWVLALELARQDHGALDCCVVVILSHGCCASHLQFFGAVYGTDCFPVSVEKIVNIENG	269
Db	94	BEIVELMRDVSKEHSHKSSFCVLLSHGEE-----GIIFGTNG-EVDLKKITNFFRG	145
Qy	270	TSCPGLGGKPKLFFFIQACGGEQKHGFEVASTSPEDSPGSGNPEPDATPFOEGLRFTDQL	329
Db	146	DRCRSLTGKPKLFIQACRGTELDGIEYDSGVDDM-----	182
Qy	330	DAISLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVEITLDDIFEQWAHSEDLQSLILRVAN	389
Db	183	-ACHKIPVEADFLYAYSTAPGYISWRNSKDGSWFIQSLCAMLKQVADKLEFMHILTRVN	241
Qy	390	AVSVK-----GIYKQMPGCENFLRKLFF	413
Db	242	KVATEFESFPDATFHAKKQIPCIVSMULTKELYF	275

Search completed: August 3, 2004, 09:08:22
Job time : 46 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:00:26 ; Search time 19 Seconds
(without alignments)

1130.337 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRRLRLVEEL.....YKQMPGCFNLRKXLPFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 352840

Minimum DB seq length: 0

Maximum DB seq length: 416

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	3	US-08-852-936C-1
2	2180	100.0	416	3	US-09-300-328-1
3	2180	100.0	416	4	US-09-069-023-23
4	2157	98.9	416	4	US-09-561-756-30
5	2157	98.9	416	4	US-09-227-721-30
6	2157	98.9	416	4	US-09-954-697-30
7	2153	98.8	416	3	US-09-257-218-2
8	2153	98.8	416	3	US-09-311-760-2
9	2153	98.8	416	4	US-08-863-579-2
10	2153	98.8	416	4	US-10-059-749-2
11	1083	49.7	203	3	US-08-852-936C-4
12	1083	49.7	203	3	US-09-300-328-4
13	418	19.2	277	3	US-08-591-605-2
14	418	19.2	277	3	US-08-964-308-6
15	418	19.2	277	3	US-08-462-969B-4
16	418	19.2	277	3	US-08-964-313-6
17	418	19.2	277	4	US-09-069-138-6
18	418	19.2	277	4	US-09-561-756-12
19	418	19.2	277	4	US-09-227-721-12
20	418	19.2	277	4	US-08-983-502-30
21	418	19.2	277	4	US-09-124-934A-4
22	418	19.2	277	4	US-08-724-378D-5
23	418	19.2	277	4	US-08-334-251D-4
24	418	19.2	277	4	US-09-516-747-30
25	418	19.2	277	4	US-09-954-697-12
26	418	19.2	277	5	PCT-US96-10521-30
27	417	19.1	277	4	US-09-291-289-11

28	409	18.8	277	2	US-08-890-542A-2	Sequence 2, Appli
29	408	18.7	277	3	US-08-964-308-10	Sequence 10, Appl
30	408	18.7	277	3	US-08-964-313-10	Sequence 10, Appl
31	408	18.7	277	4	US-09-069-138-10	Sequence 10, Appl
32	382	17.5	389	2	US-08-618-408B-4	Sequence 4, Appli
33	378	17.3	286	4	US-08-360-017-1	Sequence 1, Appli
34	371.5	17.0	335	4	US-08-983-502-16	Sequence 16, Appl
35	371.5	17.0	335	4	US-09-516-747-16	Sequence 16, Appl
36	371.5	17.0	335	5	PCT-US96-10521-16	Sequence 16, Appl
37	361.5	16.6	303	4	US-09-561-756-24	Sequence 24, Appl
38	361.5	16.6	303	4	US-09-227-721-24	Sequence 24, Appl
39	361.5	16.6	303	4	US-08-556-627A-2	Sequence 2, Appli
40	361.5	16.6	303	4	US-08-724-378D-4	Sequence 4, Appli
41	361.5	16.6	303	4	US-09-954-697-24	Sequence 24, Appl
42	361.5	16.6	303	4	US-09-163-099-2	Sequence 2, Appli
43	354.5	16.3	303	3	US-08-462-969B-2	Sequence 2, Appli
44	354.5	16.3	303	4	US-09-124-934A-2	Sequence 2, Appli
45	354.5	16.3	303	4	US-08-334-251D-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-852-936C-1
; Sequence 1, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEO for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936C
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-852-936C-1

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Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVLELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRDDQARQLII 60
    |||||
Db 1 MDEADRLRLRRCLRLVLELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRDDQARQLII 60
    |||||

QY 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
    |||||
Db 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
    |||||

QY 121 LRPEPRPVYDGGGFGDVGALSLRGADLALAYILSMFPCGHCLIIINNPNFRESGLRTR 180
    |||||
Db 121 LRPEPRPVYDGGGFGDVGALSLRGADLALAYILSMFPCGHCLIIINNPNFRESGLRTR 180
    |||||

QY 181 TGSNDCEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCVVVILSHGCO 240
    |||||
Db 181 TGSNDCEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCVVVILSHGCO 240
    |||||

QY 241 ASHLQPPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
    |||||
Db 241 ASHLQPPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
    |||||

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
    |||||
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
    |||||

QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
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Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
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RESULT 2

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US-09-300-328-1
; Sequence 1, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,328
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936
; FILING DATE: 08-MAY-1997
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-300-328-1

Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVLELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRDDQARQLII 60
    |||||
Db 1 MDEADRLRLRRCLRLVLELQVDQLWDVLLSRLFRPHMIEDIQAGSGSRDDQARQLII 60
    |||||

QY 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
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Db 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
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QY 121 LRPEPRPVYDGGGFGDVGALSLRGADLALAYILSMFPCGHCLIIINNPNFRESGLRTR 180
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Db 121 LRPEPRPVYDGGGFGDVGALSLRGADLALAYILSMFPCGHCLIIINNPNFRESGLRTR 180
    |||||

QY 181 TGSNDCEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCVVVILSHGCO 240
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Db 181 TGSNDCEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCVVVILSHGCO 240
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QY 241 ASHLQPPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
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Db 241 ASHLQPPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
    |||||

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
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Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
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QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
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Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
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RESULT 3

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US-09-069-023-23
; Sequence 23, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-23

Query Match      100.0%; Score 2180; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
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DB 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSHFHVVEKGDITAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSHFHVVEKGDITAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPAGVGTGDCPVSVSEKIVNIENGTSCLPSLGGKPKLFFFIQACGGEQKDHGFEVAS 300
DB 241 ASHLQFPAGVGTGDCPVSVSEKIVNIENGTSCLPSLGGKPKLFFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 4

US-09-561-756-30

; Sequence 30, Application US/09561756

; Patent No. 6376226

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/561,756

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 09/227,721

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-561-756-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
QY 61 DLETRGSQALPLFTISCLDGTQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFTISCLDGTQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
DB 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSHFHVVEKGDITAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSHFHVVEKGDITAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPAGVGTGDCPVSVSEKIVNIENGTSCLPSLGGKPKLFFFIQACGGEQKDHGFEVAS 300

DB 241 ASHLQFPAGVGTGDCPVSVSEKIVNIENGTSCLPSLGGKPKLFFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 5

US-09-227-721-30

; Sequence 30, Application US/09227721

; Patent No. 6379950

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/227,721

; CURRENT FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-227-721-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
QY 61 DLETRGSQALPLFTISCLDGTQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFTISCLDGTQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
DB 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSHFHVVEKGDITAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSHFHVVEKGDITAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPAGVGTGDCPVSVSEKIVNIENGTSCLPSLGGKPKLFFFIQACGGEQKDHGFEVAS 300
DB 241 ASHLQFPAGVGTGDCPVSVSEKIVNIENGTSCLPSLGGKPKLFFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 6

US-09-954-697-30

; Sequence 30, Application US/09954697

; Patent No. 6610541

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431D2

; CURRENT APPLICATION NUMBER: US/09/954,697

; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRELPRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQLPLFISCLDGTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQLPLFISCLDGTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LPETPRPVDSGGFGDVGALSLRGADLAYIILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LPETPRPVDSGGFGDVGALSLRGADLAYIILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNDCEKLRRLRRFSSPHFMEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNDCEKLRRLRRFSSPHFMEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQPPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFVEVAS 300
Db 241 ASHLQPPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFVEVAS 300
QY 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 7
US-09-257-218-2
; Sequence 2, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-257-218-2

Query Match 98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRELPRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQLPLFISCLDGTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQLPLFISCLDGTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LPETPRPVDSGGFGDVGALSLRGADLAYIILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LPETPRPVDSGGFGDVGALSLRGADLAYIILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNDCEKLRRLRRFSSPHFMEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNDCEKLRRLRRFSSPHFMEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQPPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFVEVAS 300
Db 241 ASHLQPPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFVEVAS 300
QY 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFVSWRDPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 8
US-09-311-760-2
; Sequence 2, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
; FILING DATE: 13-May-1999


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;
;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-311-760-2

Query Match          98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETRGQALPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGQALPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETPRPVDIGSGFGDVGALSLRGADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGFGDVGALSLRGADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPAGVYGTDCPVSVVEKIVNIENGTCPSLGGKPKLFFIQACGGQKHGFVEAS 300
Db 241 ASHLQFPAGVYGTDCPVSVVEKIVNIENGTCPSLGGKPKLFFIQACGGQKHGFVEAS 300
QY 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
Db 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416
Db 361 SWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416

RESULT 9
US-08-865-579-2
; Sequence 2, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-865-579-2

Query Match          98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETRGQALPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGQALPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETPRPVDIGSGFGDVGALSLRGADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPETPRPVDIGSGFGDVGALSLRGADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPAGVYGTDCPVSVVEKIVNIENGTCPSLGGKPKLFFIQACGGQKHGFVEAS 300
Db 241 ASHLQFPAGVYGTDCPVSVVEKIVNIENGTCPSLGGKPKLFFIQACGGQKHGFVEAS 300
QY 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
Db 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416
Db 361 SWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLPFKTS 416

RESULT 10
US-10-059-749-2
; Sequence 2, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/059,749
  FILING DATE: 29-Jan-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/865,579
  FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Campbell, Cathryn A.
  REGISTRATION NUMBER: 31,815
  REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (619) 535-9001
  TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 416 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match      98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRIVELOVDQLDVLRLSELFRPHMIEDIQRAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRIVELOVDQLDVLRLSELFRPHMIEDIQRAGSGSRDQARQLII 60
QY 61 DLETRGSQLPLFISCLEPTGQDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQLPLFISCLEPTGQDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPEPRPVDDIGSGFDVGALLESRGADLAYILSMPEPCGCHLINNVNFCRESGLRTR 180
Db 121 LRPEPRPVDDIGSGFDVGALLESRGADLAYILSMPEPCGCHLINNVNFCRESGLRTR 180
QY 181 TGSNDICEKLRFRFSLHFMVKGDLTAKMVLALLLELARDHGLDCCVVVILSHGCG 240
Db 181 TGSNDICEKLRFRFSPHFMVKGDLTAKMVLALLLELARDHGLDCCVVVILSHGCG 240
QY 241 ASHLQFPGAVYGTDCGCVSVEKIVNFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
Db 241 ASHLQFPGAVYGTDCGCVSVEKIVNFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
QY 301 TSPDESPGSNPEPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGVSWDRDPKSG 360
Db 301 TSPDESPGSNPEPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGVSWDRDPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKMPGCFNLRKLLFFKTS 416

RESULT 11
US-08-852-936C-4
; Sequence 4, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11

COMPUTER READABLE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/852,936C
  FILING DATE: 08-MAY-1997
  CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 60/018,961
    FILING DATE: 05-JUN-1996
    APPLICATION NUMBER: 60/020,344
    FILING DATE: 23-MAY-1996
    APPLICATION NUMBER: 60/017,949
    FILING DATE: 20-MAY-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Prestia, Paul F
    REGISTRATION NUMBER: 23,031
    REFERENCE/DOCKET NUMBER: P50483-2
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 610-407-0700
    TELEFAX: 610-407-0700
    TELEX: 846169
  INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 203 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-852-936C-4

Query Match      49.7%; Score 1083; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.8e-110;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 MVLLALLEARODHGLDCCVVVILSHGCGASHLQFPGAVYGTDCGCVSVEKIVNFNGTS 271
Db 1 MVLLALLEARODHGLDCCVVVILSHGCGASHLQFPGAVYGTDCGCVSVEKIVNFNGTS 60
QY 272 CPSLGGKPKLFFIQACGGEQKHGFVEASTSPDES PGSNPEPATPFQEGRLTFDQLDA 331
Db 61 CPSLGGKPKLFFIQACGGEQKHGFVEASTSPDES PGSNPEPATPFQEGRLTFDQLDA 120
QY 332 ISSLPTPSDIFVSYSTFPFGVSWDRDPKSGSVYVETLDDIFQWAHSEDLQSLLLRVANAV 391
Db 121 ISSLPTPSDIFVSYSTFPFGVSWDRDPKSGSVYVETLDDIFQWAHSEDLQSLLLRVANAV 180
QY 392 SVKGIYKMPGCFNLRKLLFF 413
Db 181 SVKGIYKMPGCFNLRKLLFF 202

RESULT 12
US-09-300-328-4
; Sequence 4, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
```



```
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;
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,308
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: 19840 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-7262
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-964-308-6

Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3.6e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILMEPCGHCLIIINNVPFCRSGGLRTGSGNIDCEKLRFRFSSLHFMVVKGLDTA 209
Db 34 DNSYKMDYPMGLCIIINNKNFKHKTGTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93

QY 210 KKMVLALLELARQDHGALDCCVVVILSHGCOASHLQFPFVAVYGTGDCPVSVEKIVNIENG 269
Db 94 BEIVELMRDVSKEHDKSRSSFVCLLSHGEE-----GIIFGTNG-PVDLKKIITNFRFG 145

QY 270 TSCPSLGGPKLFFITQACGGEQKHGFVASTSPEDSGSGNPEPDATPFQEGLTFDQL 329
Db 146 DRCRLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182

QY 330 DAISLPTSPDIFVSYSTFPFVSVWRDPKSGSWYVETLDDIPEQWAGHEDLQSLLRVAN 389
Db 193 -ACHKIPVEADFLYAYSTAGYYSWRNSKGSWFIQSLCAMLKQYADKLEFPHILTRVNR 241

QY 390 AVSVK-----GIYKMPGCFNFKLFF 413
Db 242 KVATFESFSDATFHAKKQIPCIIVSMLTKELYF 275
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RESULT 15
US-08-462-969B-4
; Sequence 4, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,969B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/334,251
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF140P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-462-969B-4

Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3.6e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILMEPCGHCLIIINNVPFCRSGGLRTGSGNIDCEKLRFRFSSLHFMVVKGLDTA 209
Db 34 DNSYKMDYPMGLCIIINNKNFKHKTGTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93

QY 210 KKMVLALLELARQDHGALDCCVVVILSHGCOASHLQFPFVAVYGTGDCPVSVEKIVNIENG 269
Db 94 BEIVELMRDVSKEHDKSRSSFVCLLSHGEE-----GIIFGTNG-PVDLKKIITNFRFG 145

QY 270 TSCPSLGGPKLFFITQACGGEQKHGFVASTSPEDSGSGNPEPDATPFQEGLTFDQL 329
Db 146 DRCRLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182

QY 330 DAISLPTSPDIFVSYSTFPFVSVWRDPKSGSWYVETLDDIPEQWAGHEDLQSLLRVAN 389
Db 183 -ACHKIPVEADFLYAYSTAGYYSWRNSKGSWFIQSLCAMLKQYADKLEFPHILTRVNR 241

QY 390 AVSVK-----GIYKMPGCFNFKLFF 413
Db 242 KVATFESFSDATFHAKKQIPCIIVSMLTKELYF 275
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Search completed: August 3, 2004, 09:03:39
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:07:32 ; Search time 17 Seconds
(without alignments)
2353.863 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 416
Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKQMPGCFNLRKKLFFKYS 416

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : PIR 78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	416	100.0	416	2 G02635	ICE-LAP6 - human
2	28	6.7	454	2 JC7123	caspase-9 long cha
3	9	2.2	370	2 B88455	protein T15B12.2 l
4	9	2.2	1196	2 T09356	brassinosteroid-in
5	8	1.9	232	2 A69501	hypothetical prote
6	8	1.9	324	2 AE3650	oxidoreductase (EC
7	8	1.9	368	2 T36004	hypothetical prote
8	8	1.9	372	2 G82328	aminotransferase,
9	8	1.9	579	2 T45344	hypothetical prote
10	8	1.9	752	2 T16508	hypothetical prote
11	8	1.9	787	2 T16800	hypothetical prote
12	8	1.9	758	2 T00798	hypothetical prote
13	8	1.9	794	2 T23048	hypothetical prote
14	8	1.9	1393	2 E72122	RNA polymerase bet
15	8	1.9	1393	2 B86501	RNA polymerase bet
16	8	1.9	1397	2 E81548	DNA-directed RNA p
17	7	1.7	98	2 AE2465	HicA protein (impo
18	7	1.7	132	2 T44759	glycine cleavage s
19	7	1.7	135	2 B49218	hemagglutinin homo
20	7	1.7	173	2 H90776	hypothetical prote
21	7	1.7	180	2 D86609	peptidyl-LNA hydr
22	7	1.7	180	2 E72014	peptidyl-LNA hydr
23	7	1.7	180	2 D71056	hypothetical prote
24	7	1.7	182	2 F75088	hypothetical prote
25	7	1.7	182	2 G71411	hypothetical prote
26	7	1.7	186	2 F75396	hypothetical prote
27	7	1.7	189	2 F82448	conserved hypothet
28	7	1.7	200	2 G82270	hypothetical prote
29	7	1.7	206	2 AF2299	cobalt transport A

ALIGNMENTS

RESULT 1

G02635

ICE-LAP6 - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C:Accession: G02635

R:Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,

submitted to the EMBL Data Library, April 1996

A:Reference number: H01513

A:Accession: G02635

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-416 <DUA>

A:Cross-references: EMBL:U56390; NID:gl336026; PTDN:AACS0640.1; PID:gl336027

Query Match 100.0%; Score 416; DB 2; Length 416;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60

DB 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60

hypothetical prote
hypothetical prote
hypothetical prote
probable RING zinc
transcription regu
probable hexulose-
two-component resp
conserved hypothet
hypothetical prote
hypothetical prote
nosinephide resist
probable ABC-type
methyltransferase,
ATP/GTP-binding pr
conserved hypothet
sdsB protein - Pse
ABC transporter, A
conserved hypothet
polygalacturonase-
probable membrane
hypothetical prote
hypothetical prote
hypothetical prote
transcription regu
probable anthranil
conserved hypothet
hypothetical prote
conserved hypothet
rod shape-determin
hypothetical prote
hypothetical prote
beta-lactamase-rel
hypothetical prote
RAD17 protein - ye
probable phosphopa
probable inner mem
probable transport
GTP-binding protei
sensor kinase phoQ
sensor protein pho
hypothetical prote
protein kinase pkn
GTP-binding protei
fatty acid efflux

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitens*

A;Reference number: AD3252; PMID:11756688

A;Accession: AE3650

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-324 <KUR>

A;Cross-references: GB:AE008918; PIDN:AA154368.1; PID:gl17985352; GSPDB:GN00191

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEI1126

A;Map position: II

C;Keywords: oxidoreductase

Query Match 1.9%; Score 8; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARQ 222
|||||||
DB 103 ALLELARQ 110

RESULT 7

T36004

hypothetical protein SCC22.14c - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000

C;Accession: T36004

R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999

A;Reference number: Z21574

A;Accession: T36004

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-368 <SEE>

A;Cross-references: EMBL:AL096839; PIDN:CAB50757.1; GSPDB:GN00070; SCOEDB:SCC22.14c

C;Genetics:

A;Gene: SCOEDB:SCC22.14c

C;Superfamily: Streptomyces coelicolor hypothetical protein SCC22.14c

Query Match 1.9%; Score 8; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EADRRLLR 10
|||||||
DB 81 EADRRLLR 88

RESULT 8

G82328

aminotransferase, class V VC0392 [imported] - *Vibrio cholerae* (strain N16961 serogroup O)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: G82328

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Hirschman, D.; Ermlaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragoi, I.; Sellers, F.L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: G82328

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-372 <HEI>

A;Cross-references: GB:AE004127; GB:AE003852; NID:g9654808; PIDN:AAF93565.1; GSPDB:GN001

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0392

A;Map position: 1

C;Superfamily: serine-pyruvate aminotransferase

Query Match 1.9%; Score 8; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GCFVSVEK 262
|||||||

DB 119 GCFVSVEK 126

RESULT 9

T45344

hypothetical protein MLCB57.28c [imported] - *Mycobacterium leprae*

C;Species: *Mycobacterium leprae*

C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 28-Jul-2000

C;Accession: T45344

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z16918

A;Accession: T45344

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-579 <PAR>

A;Cross-references: EMBL:Z99494; PIDN:CAB16668.1

A;Experimental source: cosmid B57

C;Genetics:

A;Note: MLCB57.28c

C;Superfamily: *Mycobacterium leprae* hypothetical protein MLCB57.28c

Query Match 1.9%; Score 8; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GLRTRTGS 183
|||||||

DB 17 GLRTRTGS 24

RESULT 10

T16508

hypothetical protein F59A6.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T16508

R;Nhan, M.

submitted to the EMBL Data Library, December 1995

A;Description: the sequence of *C. elegans* cosmid F59A6.

A;Reference number: Z18526

A;Accession: T16508

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-752 <NHA>

A;Cross-references: EMBL:U41994; NID:gl123047; PID:gl123051; PIDN:AAA83455.1; CESP:F59A6

C;Genetics:

A;Gene: CESP:F59A6.4

A;Introns: 43/3; 146/3; 334/1; 400/3; 433/2; 515/3; 672/1

Query Match 1.9%; Score 8; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
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DB 441 GSGGFGDV 448

RESULT 11

T16800

hypothetical protein T05A7.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: TL6800
R;Chisoe, S.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid T05A7.
A;Reference number: Z18580
A;Accession: TL6800
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-758 <CHI>
A;Cross-references: EMBL:U40028; NID:g1055143; PID:g1055145; PIDN:AAA81115.1; CESP:T05A7
C;Genetics:
A;Gene: CESP:T05A7.6
A;Introns: 41/3; 142/3; 330/1; 396/3; 439/2; 678/1

Query Match 1.9%; Score 8; DB 2; Length 758;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGDV 139
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Db 447 GSGGFGDV 454

RESULT 12
T00798
hypothetical protein At2g32700 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F24L7.16
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T00798; D84736
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, February 1998
A;Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence.
A;Reference number: Z14204
A;Accession: T00798
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-787 <ROU>
A;Cross-references: EMBL:AC003974; NID:g2914688; PID:g2914703
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84736
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-787 <STO>
A;Cross-references: GB:AB002093; NID:g2914703; PIDN:AAC04493.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g32700; F24L7.16
A;Map position: 2
A;Introns: 11/2; 44/1; 80/3; 174/2; 200/3; 238/1; 254/3; 347/3; 372/3; 448/3; 497/1; 533

Query Match 1.9%; Score 8; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 FGDVGALE 143
|||||
Db 456 FGDVGALE 463

RESULT 13
T23048
hypothetical protein H05L14.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T23048; T25112
R;Barlow, K.
submitted to the EMBL Data Library, October 1997

A;Reference number: Z19662
A;Accession: T23048
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-794 <WIL>
A;Cross-references: EMBL:Z99772; PIDN:CAB16921.1; GSPDB:GN00019; CESP:H05L14.1
A;Experimental source: clone H05L14
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19982
A;Accession: T25112
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-794 <WT2>
A;Cross-references: EMBL:Z75550; PIDN:CAA99932.1; GSPDB:GN00019; CESP:H05L14.1
A;Experimental source: clone T22C1
C;Genetics:
A;Gene: CESP:H05L14.1
A;Map position: 1
A;Introns: 8/1; 61/3; 147/3; 196/3; 231/3; 354/1; 383/2; 437/2; 584/3; 635/3; 658/3; 70

Query Match 1.9%; Score 8; DB 2; Length 794;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGDV 139
|||||
Db 468 GSGGFGDV 475

RESULT 14
E72122
RNA polymerase beta' - Chlamydomophila pneumoniae (strain CWL029)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: E72122
R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: E72122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1393 <ARN>
A;Cross-references: GB:AE001593; GB:AE001363; NID:g4376334; PIDN:AAD18235.1; PID:g43763
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: rpoC
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1393;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 SEDLQSL 384
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Db 194 SEDLQSL 201

RESULT 15
B86501
RNA polymerase beta' [imported] - Chlamydomophila pneumoniae (strain J138)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: B86501
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: B86501
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1393 <STO>

A;Cross-references: GB:BA000008; NID:g8978455; PIDN:BAA98292.1; GSPDB:GN00142
 A;Experimental source: strain J138
 C;Genetics:

C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1393;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SEDLQSL 384
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 Db 194 SEDLQSL 201

RESULT 16

E81548
 DNA-directed RNA polymerase, beta' chain CP0693 [imported] - Chlamydomonadales pneumoniae (s

C;Species: Chlamydomonadales pneumoniae, Chlamydia pneumoniae
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
 C;Accession: E81548

R;Read, I.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Winn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81548

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1397 <REA>

A;Cross-references: GB:AE002228; GB:AE002161; NID:g7189606; PIDN:AAF38501.1; PID:g718960

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CP0693

C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1397;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SEDLQSL 384
 |||||
 Db 198 SEDLQSL 205

RESULT 17

AE2465

H1A protein [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AE2465

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2465

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <KUR>

A;Cross-references: GB:BA000019; PIDN:BAE76976.1; PID:gl7134416; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: asl5277

Query Match 1.7%; Score 7; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TLDDIFE 372
 |||||
 Db 10 TLDDIFE 16

RESULT 18

T44759

glycine cleavage system protein H [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000

C;Accession: T44759

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, October 1997

A;Reference number: Z22833

A;Accession: T44759

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-132 <PAR>

A;Cross-references: EMBL:AL008609; PIDN:CAA15469.1

A;Experimental source: cosmid B1768

C;Genetics:

A;Gene: gcvH

C;Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology

Query Match 1.7%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 DVGAL 144
 |||||
 Db 109 DVGAL 115

RESULT 19

B49218

hemagglutinin homolog pmGAL.3 - Mycoplasma gallisepticum (fragment)

C;Species: Mycoplasma gallisepticum

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 07-Dec-1999

C;Accession: B49218

R;Markham, P.F.; Glew, M.D.; Whithear, K.G.; Walker, I.D.

Infect. Immun. 61, 903-909, 1993

A;Title: Molecular cloning of a member of the gene family that encodes pmGA, a hemagglut

A;Reference number: A49218; MUID:93162830; PMID:8432610

A;Accession: B49218

A;Status: preliminary

A;Molecule type: DNA; protein

A;Residues: 1-135 <MAR>

A;Cross-references: GB:S55216; NID:g265625; PIDN:AAB25398.1; PID:g265627

A;Experimental source: S6

A;Note: sequence extracted from NCBI backbone (NCBIN:125182, NCBIP:125184)

C;Genetics:

A;Genetic code: SGC3

Query Match 1.7%; Score 7; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TLENLTP 108
 |||||
 Db 129 TLENLTP 135

RESULT 20

H90776

hypothetical protein ECs1184 [imported] - Escherichia coli (strain O157:H7, substrain R11

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C;Accession: H90776

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iihii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: H90776

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-173 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BA834607.1; PID:q13360644; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain RMD 050952
 C;Genetics:
 A;Gene: ECs1184

Query Match 1.7%; Score 7; DB 2; Length 173;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 PVLRPE 114
 |||||
 Db 134 PVLRPE 140

RESULT 21

D86609 peptidyl tRNA hydrolase [imported] - Chlamydomophila pneumoniae (strain J138)

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C;Accession: D86609

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: D86609

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-180 <STO>

A;Cross-references: GB:BA000008; NID:98979324; PIDN:BAA99158.1; GSPDB:GN00142

A;Experimental source: strain J138

C;Genetics:

A;Gene: pth

C;Superfamily: peptidyl-tRNA hydrolase

Query Match 1.7%; Score 7; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLVEELQ 21
 |||||
 Db 29 RLVEELQ 35

RESULT 22

E72014 peptidyl-tRNA hydrolase CP0909 [imported] - Chlamydomophila pneumoniae (strains CWL029 and

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C;Accession: E72014; G81523

R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: E72014

A;Molecule type: DNA

A;Residues: 1-180 <ARN>

A;Cross-references: GB:AE001675; GB:AE001363; NID:g4377273; PIDN:AAD19088.1; PID:g437727

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: G81523

A;Molecule type: DNA

A;Residues: 1-180 <REA>

A;Cross-references: GB:AE002250; GB:AE002161; NID:g7189821; PIDN:AAF38694.1; PID:g718982

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: pth; CP0909

C;Superfamily: peptidyl-tRNA hydrolase

Query Match 1.7%; Score 7; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLVEELQ 21
 |||||
 Db 29 RLVEELQ 35

RESULT 23

F71056

hypothetical protein PH1148 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000

C;Accession: F71056

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: F71056

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-180 <KAW>

A;Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30248.1; PID:g3257565

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH1148

Query Match 1.7%; Score 7; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 ALLELAR 221
 |||||
 Db 174 ALLELAR 180

RESULT 24

D75088

hypothetical protein PAB0726 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: D75088

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A;Reference number: A75001

A;Accession: D75088

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-182 <KAW>

A;Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50009.1; PID:g545836

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB0726

Query Match 1.7%; Score 7; DB 2; Length 182;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 ALLELAR 221
 |||||
 Db 176 ALLELAR 182

RESULT 25

G71411

hypothetical protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

A;Variety: columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

C;Accession: G71411
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirkx, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Fohl, T.M.; Terryn, N.; Gielanagh, T.; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana
A;Reference number: A71400; MUID:96121113; PMID:9461215
A;Accession: G71411
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-182 <BEV>
A;Cross-references: GB:297337; NID:g2244829; PID:e326833; PID:g2244843
C;Genetics:
A;Map position: 4COP9-4G3845

Query Match 1.7%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 NFLRKKL 411
|||||
DB 3 NFLRKKL 9

RESULT 26
S73396
hypothetical protein c04030 - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 17-Mar-1999
C;Accession: S75396
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S. Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: the Sulfolobus solfataricus genome
A;Reference number: S73076; MUID:97055432; PMID:8999719
A;Accession: S75396
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-186 <SEN>
A;Cross-references: EMBL:Y08257; NID:g1707772; PID:e283882; PID:g1707802
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996

Query Match 1.7%; Score 7; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 LFIISCLE 78
|||||
DB 42 LFIISCLE 48

RESULT 27
F82448
conserved hypothetical protein VCA0539 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82448
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <HEI>
A;Cross-references: GB:AE004384; GB:AE003853; NID:g9657936; PIDN:AAF96441.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:

A;Gene: VCA0539
A;Map position: 2

Query Match 1.7%; Score 7; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 EVKGDLT 208
|||||
DB 121 EVKGDLT 127

RESULT 28

G82270
hypothetical protein VC0859 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82270
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <HEI>
A;Cross-references: GB:AE004171; GB:AE003852; NID:g9655308; PIDN:AAF94021.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0859
A;Map position: 1

Query Match 1.7%; Score 7; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 EDIQRAG 47
|||||
DB 67 EDIQRAG 73

RESULT 29
AF2299
cobalt transport ATP-binding protein cbiO [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF2299
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA075648.1; PID:g17133083; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: cbiO
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7%; Score 7; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 RDOARQL 58
|||||
DB 83 RDOARQL 89

RESULT 30
E83859
hypothetical protein BH1677 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E83859
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E83859
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <STO>
A;Cross-references: GB:AP001512; GB:BA000004; NID:gl0174030; PIDN:BAB05396.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1677
C;Superfamily: conserved hypothetical protein TM1511

Query Match 1.7%; Score 7; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLBLAR 221
|||||
Db 207 ALLBLAR 213

RESULT 31
T51025
hypothetical protein B7F21.60 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
C;Accession: T51025
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25286
A;Accession: T51025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <SCH>
A;Cross-references: EMBL:AL389901; GSPDB:GN00116; NCSP:B7F21.60
A;Experimental source: BAC clone B7F21; strain OR74A
C;Genetics:
A;Gene: NCSP:B7F21.60
A;Map position: 6
A;Introns: 16/1; 55/2; 70/3; 129/2; 179/3; 196/1
C;Superfamily: Neurospora crassa hypothetical protein B7F21.60

Query Match 1.7%; Score 7; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 QAGKLSK 100
|||||
Db 137 QAGKLSK 143

RESULT 32
T13312
hypothetical protein 23 - Streptococcus phage phi-O1205
C;Species: Streptococcus phage phi-O1205
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 18-Aug-2000
C;Accession: T13312
R;Stanley, E.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.
Microbiology 143, 3417-3429, 1997
A;Title: Sequence analysis and characterization of phi O1205, a temperate bacteriophage
A;Reference number: Z17654; MUID:98048466; PMID:9387220
A;Accession: T13312
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-236 <STA>
A;Cross-references: EMBL:U88974; NID:g2444080; PID:g2444103; PIDN:AAC79539.1
A;Experimental source: host Streptococcus thermophilus strain CNRZ1205
C;Superfamily: Streptococcus phage phi-O1205 hypothetical protein 23

Query Match 1.7%; Score 7; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LLSRELF 35
|||||
Db 177 LLSRELF 183

RESULT 33

G84678

probable RING zinc finger protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84678

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84678

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <STO>

A;Cross-references: GB:AF002093; NID:g4510422; PIDN:AD21508.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g27940

A;Map position: 2

Query Match 1.7%; Score 7; DB 2; Length 237;

Best Local Similarity 100.0%; Pred. No. 80;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 QACGGEQ 291

Db 14 QACGGEQ 20

RESULT 34

DB7435

transcription regulator, AraC family [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C;Accession: D87435

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolc

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: D87435

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-240 <STO>

A;Cross-references: GB:AE005673; NID:gl3422878; PIDN:AAK23480.1; GSPDB:GN00148

C;Genetics:

A;Gene: CC1501

Query Match 1.7%; Score 7; DB 2; Length 240;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 FGDVGAL 142

Db 73 FGDVGAL 79

```

RESULT 35
H72691
C:probable hexulose-6-phosphate synthase APE0952 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H72691
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72691
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-241 <RAW>
A:Cross-references: DDBJ:AF000060; NID:G5104186; PIDN:BAA79936.1; PID:d1043722; PID:g510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0952

Query Match 1.7%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALESRLG 147
Db 229 ALESRLG 235

RESULT 36
C82995
two-component response regulator OmpR PA5200 [imported] - Pseudomonas aeruginosa (strain
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C82995
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C82995
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <STO>
A:Cross-references: GB:AE004933; GB:AE004091; NID:g9951505; PIDN:AA08585.1; GSPDB:GN004
A:Experimental source: strain PA01
C:Genetics:
A:Gene: ompR; PA5200
C:Superfamily: ompR protein; response regulator homology

Query Match 1.7%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LLSRELF 35
Db 49 LLSRELF 55

RESULT 37
E69455
conserved hypothetical protein AF1646 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: E69455
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

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A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69455
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <KLE>
A:Cross-references: GB:AE000989; GB:AE000782; NID:g2689312; PIDN:AAB89596.1; PID:g264890

Query Match 1.7%; Score 7; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 KPTLENL 106
Db 187 KPTLENL 193

RESULT 38
T18886
hypothetical protein C03D6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18886
R;Burton, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19038
A:Accession: T18886
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-262 <WIL>
A:Cross-references: EMBL:Z75525; PIDN:CAA99766.1; GSPDB:GN000019; CESP:C03D6.1
A:Experimental source: clone C03D6
C:Genetics:
A:Gene: CESP:C03D6.1
A:Map position: 1
A:Introns: 21/2; 58/3; 125/3; 229/2

Query Match 1.7%; Score 7; DB 2; Length 262;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 FNGTSCP 273
Db 61 FNGTSCP 67

RESULT 39
T06613
hypothetical protein F16J13.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C:Accession: T06613
R;Revan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15789
A:Accession: T06613
A:Molecule type: DNA
A:Residues: 1-267 <BEV>
A:Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.130
A:Experimental source: cultivar Columbia; BAC clone F16J13
C:Genetics:
A:Gene: ATSP:F16J13.130
A:Map position: 4
A:Introns: 80/2; 93/2; 130/1; 190/1; 228/2

Query Match 1.7%; Score 7; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 AISSLPT 337
Db 73 AISSLPT 79

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RESULT 40
JQ0686
nosiheptide resistance protein - Streptomyces actuosus
C;Species: Streptomyces actuosus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 17-Mar-2000
C;Accession: JQ0686
R;Li, Y.; Dosch, D.C.; Strohl, W.R.; Floss, H.G.
Gene 91, 9-17, 1990
A;Title: Nucleotide sequence and transcriptional analysis of the nosiheptide-resistance
A;Reference number: JQ0685; MUID:90382703; PMID:2401410
A;Accession: JQ0686
A;Molecule type: DNA
A;Residues: 1-274 <LI>
A;Cross-references: GB:U75434; GB:M32744; NID:g1654409; PIDN:AAB17875.1; PID:g1654411
A;Experimental source: ATCC 25421
C;Genetics:
A;Gene: nsh
C;Superfamily: conserved hypothetical protein HI0860
C;Keywords: antibiotic resistance

Query Match      1.7%; Score 7; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 ADRRLR 10
      |||||
Db     156 ADRLLR 162

RESULT 41
T36288
probable ABC-type transport system ATP-binding chain - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: T36288
R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21603
A;Accession: T36288
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-276 <SEE>
A;Cross-references: EMBL:AL049819; PIDN:CAB42665.1; GSPDB:GN000070; SCOEDB:SCE7.06C
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE7.06C
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match      1.7%; Score 7; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy     177 LRRTGS 183
      |||||
Db     243 LRRTGS 249

RESULT 42
E87682
methyltransferase, UbiE/COQ5 family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87682
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87682
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <STO>

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A;Cross-references: GB:AE005673; NID:g13425221; PIDN:AAK25457.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3495

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Query Match      1.7%; Score 7; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     215 ALLELR 221
      |||||
Db     81 ALLELR 87

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RESULT 43

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B97536
ATP/GTP-binding protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: B97536
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87243.1; PID:gl5156529; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 2676
A;Map position: circular chromosome

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Query Match      1.7%; Score 7; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 EADRRLL 9
      |||||
Db     10 EADRRLL 16

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RESULT 44

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G71276
conserved hypothetical protein TP0829 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: G71276
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: G71276
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-294 <COL>
A;Cross-references: GB:AE001253; GB:AE000520; NID:g3323133; PIDN:AAC65795.1; PID:g33231
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0829

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Query Match      1.7%; Score 7; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     216 LLELARQ 222
      |||||
Db     272 LLELARQ 278

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RESULT 45

JC1120

sdsB protein - Pseudomonas sp.
A;Species: Pseudomonas sp.
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 24-Nov-1999
C;Accession: JC1120
R;Davison, J.; Brunel, F.; Phanopoulos, A.; Prozzi, D.; Terpetra, P.
Gene 114, 19-24, 1992
A;Title: Cloning and sequencing of Pseudomonas genes determining sodium dodecyl sulfate
A;Reference number: JC1118; MUID:92267380; PMID:1587481
A;Accession: JC1120
A;Molecule type: DNA
A;Residues: 1-306 <DNA>
A;Cross-references: GB:M86744; NID:g151550; PIDN:AAA25988.1; PID:g151551
C;Genetics:
A;Gene: sdsB
C;Superfamily: conserved hypothetical protein HI1364

Query Match 1.7%; Score 7; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELA 220
|||||||
Db 256 LALLELA 262

RESULT 46

D75447
ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75447
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <WHI>
A;Cross-references: GB:AE001953; GB:AE000513; NID:g6458740; PIDN:AAF10588.1; PID:g645874
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1012
A;Map position: 1
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7%; Score 7; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 VLALLEL 219
|||||||
Db 125 VLALLEL 131

RESULT 47

G64456
conserved hypothetical protein MJ1256 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: G64456
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.L.; Overberg, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: G64456
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-311 <BUL>
A;Cross-references: GB:U67566; GB:L77117; NID:g1591887; PIDN:AAB99260.1; PID:g1591890; T
C;Genetics:
A;Map position: FOR1198613-1199548
A;Start codon: GTG
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1256

Query Match 1.7%; Score 7; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 VSVKGIV 397
|||||||
Db 251 VSVKGIV 257

RESULT 48

S60713
polygalacturonase-inhibiting protein - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 17-Mar-1999
C;Accession: S60713
R;Favaron, F.; D'Ovidio, R.; Porceddu, E.; Alghisi, P.
Planta 195, 80-87, 1994
A;Title: Purification and molecular characterization of a soybean polygalacturonase-inhi
A;Reference number: S60713; MUID:95152348; PMID:7765794
A;Accession: S60713
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <FAV>
A;Cross-references: EMBL:X78274; NID:g809547; PID:g809548
C;Superfamily: polygalacturanase-inhibiting protein; leucine-rich alpha-2-glycoprotein r

Query Match 1.7%; Score 7; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 PSLGGKP 279
|||||||
Db 191 PSLGGKP 197

RESULT 49

AB0350
probable membrane protein YPO2874 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AB0350
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92125.1; PID:g15980841; GSPDB:GN00175
C;Genetics:
A;Gene: YPO2874

Query Match 1.7%; Score 7; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLRRCL 14
|||||||
Db 25 LLRRCL 31

RESULT 50

A72637
hypothetical protein APE1552 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: A72637
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; X
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <KAW>
A:Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80551.1; PID:d1044337; PID:g510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1552

Query Match 1.7%; Score 7; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AGSGSRR 52
|||
DB 306 AGSGSRR 312

Search completed: August 3, 2004, 09:11:13
JOB time : 21 secs